Page 1

Run on: OM protein - protein search, using sw model February Copyright 9, 2005, 23:46:53 ; Search time 40 Seconds (without alignments) 921.276 Million cell updates/sec GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

Title: Perfect score: US-10-056-405-2 383 1 MYYNFKVFKKCAPNGKVTLY.......

.ADVETFRQDTIDQQASVDFE 383

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size :

Total number of hits satisfying chosen parameters: 283416

Minimum | Maximum | DB seq length: 0
DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_79:*

pir1: pir2: pir3:*

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being present is derived by analysis of the total score distribution.

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ALIGNMENTS

¥ A;Cross-references: UNIPROT:P15372; GB:M30177
R;Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vihtelic, T.S.; Benzer, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1008-1012, 1990
A;Title: Twenty Drosophila visual system cDNA clones: one is a homolog of human arresti. A;Reference number: A34868; MUID:90138926; PMID:2105491
A;Accession: A34868 R;Smith, D.P.; Shieh, B.H.; Zuker, C.S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1003-1007, 1990
A;Title: Isolation and structure of an arrestin gene from Drosophila.
A;Reference number: A34867; MUID:90138925; PMID:1689056
A;Accession: A34867 arrestin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Jul1-1990 #sequence revision 20-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34867; A34868 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-364 <HYD> A;Cross-references: GB:M30140; NID:g156961; PIDN:AAA28380.1; PID:g156962 A; Molecule type: DNA A; Residues: 1-364 < SMI> A; Status: preliminary

밁 S 228 VKKIKAMVQQGVDVVLFQNG 247 227 VKKIKAMVOOGVDVVLFONG 246

Matches Query Match Local

l Similarity 20; Conserv

5.2%; Score 20; DB ilarity 100.0%; Pred. No. 3e-Conservative 0; Mismatches

DB 2; Length 364; 3e-12;

Indels

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A;Gene: PlyBase:Arr1
A;Cross-references: PlyBase:FBgn0000120
A;Introns: 36/3; 306/3; 349/3
C;Superfamily: arrestin

arreshin 1 - bluebottle fly (Calliphora vicina) C;Speches: Calliphora vicina

C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004 c;Accession: A55081; 844291 R;Plangger A.; Malicki, D.; Whitney, M.; Paulsen, R. J. Biol. Chen. 269, 26969-26975, 1994 A;Title: Mechanism of arrestin 2 function in rhabdomeric photoreceptors. A;Reference number: A55081; MUID:95014564; PMID:7929436 A;Accession: A55081 MUID:95014564; PMID:7929436 A;Status: prelimbary

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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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arrestin homolog -
arrestin homolog -
nitrogen fixation
protein-tyrosine |
E5 protein - human
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RESULT A55081 arrest C;Pace C;Pace C;Pace R;Plan J, Bio A;Titl A;Refe A;Acce A;Stat	Que Bes Mat Qy Db	A; Status A; Molecu A; Residu A; Cross C; Geneti A; Gene: 1 A; Cross A; Intron C; Superf	A,Status A,Molecu A,Residus A,Cross R,Hyde, T Proc. Nat Prot. Nat A,Title: A,Referer A,Recessa	RESULT 1 A34867 A34867 Arrestin C;Specie: C;Access: R;Smith, Proc. Nat A;Title: A;Access:		
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ily (Calliphora ina ence_revision 91; Whitney, M 1-26975, 1994 restin 2 functi	5.2%; S 100.0%; tive 0; VDVVLFQNG 	0140; 8e:FBg	(OT:P15372), K.L.; Pc S.A. 87, : a visual :	UII ek		92 2 BI 1139 2 SI 1139 2 BI 1139 2 BI 1145 2 C PA 1155 2 PA 1156 2 PA 1166 2
lliphora vicina) svision 03-Aug-1995 #text_chan (they, M.; Paulsen, R. 1994 function in rhabdomeric photol)	Pred. No. 3e-12; Length Pred. No. 3e-12; Inde Mismatches 0; Inde 247	961; PIDN:AAA28380.1	cy MI MIPROT:P15372; GB:M30177 UNIPROT:P15372; GB:M30177 LI, L, S, P0llock, J.A.; Vihtelic, T MI, S, A. 87, 1008-1012, 1990 Sophila visual system cDNA clones: one i A34868; MUID:90138926; PMID:2105491 , C,	ogaster) 20-Jul-1990 #text_c 20-Jul-1990 #text_c -1007, 1990 arrestin gene from 925; PMID:1689056	ALIGNMENTS	B82603 S10222 E97426 E97426 A82644 A826447 A83639 C64447 A83639 C81877 A27873 A27873 A27873 A27873 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969 A35969
ange 09-Jul-2004 Octoreceptors.	364; :ls 0; Gaps	; PID:9156962	.S.; Benzer, S. s a homolog of	_change 09-Jul-2004 n Drosophila.		hypothetical prote hypothetical prote flagellar basal-bo classive prote plagellar basal-bo conserved hypothetical prote hypothetical prote osmotically induci hypothetical prote allophycocyanin al hypothetical prote carQ protein - Myx glycoprotein - Myx glycoprotein - Mypothetical prote carQ protein - Myx glycoprotein - Myx glycoprotei
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arrestin

Matches

Similarity

Score 17;

Length 363;

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49K photoreceptor protein - fruit fly (Drosophila melanogaster)
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C;Species: Locusta migratoria (migratory locust)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: A56807
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Best Local :
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                                                                                                                                                                                                                                   Residues: 1-407 <RAM>
                                                                                                                                                                                                                                                                            "Reill Signal 5, 69-80, 1993"
"Title: Arrestin-subtypes in insect antennae."
"Contents: antennae A56607; MUID:93199955; PMID:8452755; Scatter. 3-56607; Scatter. 3-56607; Scatter. 3-56607; Scatter. 3-56607; Scatter. 3-56607; Scatter. 3-56607; MUID:93199955; PMID:8452755; Scatter. 3-56607; MUID:93199955; PMID:8452755; Scatter. 3-56607
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A;Ressidues: 1-381 <RAM>
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A;Reference number: A56607; MUID:93199955; PMID:8452755
A;Accession: B56607
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C.Species: Heliothis virescens (tobacco budworm)
C.Pate: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
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Experimental source: antennae

Note: sequence extracted from NCBI backbone (NCBIP:127926)
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A;Residues: 1-363 <PLA>
A;Cross-references: UNIPROT:P51486; GB:X79072; NID:9483527; PIDN:CAA55672.1; PID:9483528
A;Note: the source is designated as Calliphora erythrocephala
         A;Note: the source is de C;Superfamily: arrestin
                A;Cross-references: UNIPROT:P51487;
A;Note: the source is designated as
                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-401 <PLA>
                                                                        R;Planger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
Biol. Chem. 269, 26969-26975, 1994
A;Title: Mechanism of arrestin 2 function in rhabdomeric photoreceptors.
A;Reference number: A55081; MUID:95014564; PMID:7929436
                                                                                                                                                     arrestin 2 - bluebottle fly (Calliphora vicina)
C.Species: Calliphora vicina
C.Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
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A;Cross-references: FlyBase:FBgn0012552
A;Introns: 286/1; 351/1
C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Residues: 1-401 <KRI>A)CTOSS-TEFERENCES: UNIDROT:P19108; EMBL:X54084; NID:g7612; PIDN:CAA38019.1; PID:g295739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYKIShnan, R; Ganguly, R.
Nucleic Acids Res. 18, 5894, 1990
A;Title: Nucleotide sequence of the arrestin-like 49 Kd
A;Reference number: S11566; MUID:91016944; PMID:2216789
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A;Residues: 1-401 <K
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C;Speciaes: Drosophila miranda
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11566
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C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C;Accession: A3485
R;Yamada, T; Takeuchi, Y.; Komori, N.; Kobayashi, H.; Sakai, Y.; Hotta, Y.; Matsumot Science 248, 483-485, 1990
A;Title: A 49-kilodalton phosphoprotein in the Drosophila photoreceptor is an arrestian arrestian arrestian arrestian arrestian.
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C;Superfamily: arrestin
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A;Rolecule type: mRNA
A;Residues: 1-401 <YAM>
A;Cross-references: UNIPROT:P19107; GB:M32141; NID:g158157; PIDN:AAA28833.1; PID:g1581
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Calliphora erythrocephala
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PIDN:CAA55673.1; PID:g48356
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arrestin - human (fragment)
C;Species: Homo espiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
C;Accession: S18984
R;Rapoport, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arrestin isoform 15, erythrocyte - rainbow trout C;Species: Oncorhynchus mykiss (rainbow trout) C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S68253 R;Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motais, R.; Fievet, B. Blochem. J. 316, 497-506, 1996 A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin A;Reference number: S68253; MUID:96257743; PMID:8687393 A;Accession: S68253 A;Status: preliminary; nucleic acid sequence not shown
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A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrangement of the arrangement of the property of the propert
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C;Date: O6-Dec-1996 #sequence_revision 13-Mar-1997
C;Accession: $68254
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A;Residues: 1-405 <JAH>
A;Cross-references: UNIPROT:P51467; GB:U48410
submitted to the EMBL Data Library, A;Description: Isolation of a novel A;Reference number: S18984 A;Accession: S18984
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A;Residues: 1-407 <JAH>
A;Cross_references: UNIPROT:P51466;
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Pred. No.
                                                      November 1991 cDNA belonging
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-320,'A',322-325,'A',327-330,'A',332-410 <AT2>
A;Cross-references: GB:M91590; NID:g949986
A;Note: sequence extracted from NCBI backbone (NCBIP:112790)
A;Note: the sequence is revised in GenBank entry RATBARRES2, release 113.
A;Note: the sequence is revised in GenBank entry RATBARRES2, release 113.
B;Cross-residue (C.M.; Whitmore, D.H.; 1994
A;Title: Cone arrestin identified by targeting expression of a functional
A;Reference number: I55423; MUID:94140898; PMID:8308033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P29067; GB:M91590; NID:g949986; PIDN:AAA74460.1; PID:g203104
A;Experimental source: strain Sprague-Dawley; stage adult; tissue type brain; tissue lib
R;Attramadal, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder
J. Biol. Chem. 267, 17882-17890, 1992
A;Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene family.
A;Reference number: A43404; MUID:92388146; PMID:1517224
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A;Reference number: S68253; MUID:96257743; PMID:8687393 A;Accession: S68255 A;Status: preliminary; nucleic acid sequence not shown
                                                                    R;Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Mot
Biochem. J. 316, 497-506, 1996
A;Title: Trout red blood cell arrestin (TRCarr), a novel
                                                                                                                                          arrestin isoform 1L, erythrocyte - rainbow trout C;Species: Oncorhynchus mykiss (rainbow trout) C;Date: 06-Dec-196 #sequence_revision 13-Mar-1997 #text_change C;Accession: S68255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U03627; NID:g458202; PIDN:AAA17551.1; PID:g458203 C;Superfamily: arrestin
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C;Species: Rat
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A;Residues: 1-409 <RAP>
A;Cross-references: UNIPROT:P32121; EMBL:Z11501; NID:g28850; PIDN:CAA77577.1; PID:g28851
C;Superfamily: arrestin
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A; Residues: 295-410 < CRA>
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A; Residues: 1-410 < ATT>
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                           member of
                                                                                                                         R.; Fievet,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.; Kwatra,
                                                                                                                                                                         09-Jul-2004
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Query Match
Best Local Similarity
Thes 9; Conserve
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A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: EMBL:U03626; NID:9458200; PID:9-
C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                                                                        arrestin-C - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 13-Sep-1998
C;Accession: I55423 #sequence_revision 24-May-1996 #text_change 13-Sep-1998
R;Craft, C.M.; Whitmore, D.H.; Wiechmann, A.F.
J. Biol. Chem. 269, 4613-4619, 1994
A;Title: Cone arrestin identified by targeting expression of a functional family.
A;Accession: I55423; MUID:94140898; PMID:8308033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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A;Accession: B47140
A;Mccession: B47140
A;Mccession: B47140
A;Mccession: B47140
A;Mccession: By A;Mccession: By B;Mcaller 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P32120; GB:L14641
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:136006, NCBIP:136007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arrestin arr3L - bovine
N;Contains: arrestin arr3S
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Feb-1994 #8equence revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47140; B47140; JC2051
J. Biol. C;Dem. 268, 15640-15648, 1993
A;Title: Polypeptide variants of beta-arrestin and arrestin3.
A;Reference number: A47140; MUID:93340166; PMID:8340388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-420 <STE>
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A; Residues: 1-415 < JAH>
A; Cross-references: UNIPR
C; Superfamily: arrestin
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GKRDFVDHV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Conservative 0; Mismatc
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                                                                                                                                                                                                                   EMBL:U03626; NID:g458200; PID:g458201
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Conservative 0; Mismatches 0;
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                                                                                              Mismatches
                                                                                                              DB 2;
lo. 0.76;
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                                                                        R;Murakami, A.; Yajima, T.; Sakuma, H.; McLaren, M.J.; Inana, G. PEBS lett. 334, 203-209, 1993
A;Title: X-arrestin: a new retinal arrestin mapping to the X chromosome. A;Reference number: S38943; MUID:94039835; PMID:8224247
                                                                                                                                                                                                   Cripecies: Homo sapiens (man)
Cripecies: Homo sapiens (man)
Cripate: 19-May-1994  #sequence_revision 17-Nov-1995  #text_change 09-Jul-2004
Cripacession: S33943  #sequence_revision 17-Nov-1995  #text_change 09-Jul-2004
                                     Query Match

Best Local Similarity 2.3%; Score 9; DB 2

Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                   RESULT 15
838943
19 GKRDFVDHV 27
                   22 GKRDFVDHV 30
                                                DB 2;
lo. 0.76;
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                                                        Length 388;
                                  Indels
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                            Gaps
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Search completed: February 10, Job time : 42 secs 2005, 00:02:18

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Maximum Match 100%
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Maximum DB seq length: 2000000000
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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4: pir4:*
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1 MVYNFKVFKKCAPN
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Gapop 10.0 , Gapext 0.5
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                                    MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQQASVDFE 383
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        GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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        N34867
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N44856
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N45081
N55081
N568255
N56825
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cone arrestin - no

s-antigen - mouse

arrestin - human

s-antigen - rat

s-antigen - bovine

retinal S-antigen

rod arrestin - nor

arrestin-C - human

rod arrestin - bul

C-arrestin - rat (
                                                                                                                                                                                                                 hypothetical prote
arrestin isoform 1
arrestin isoform 2
cone arrestin - Af
cone arrestin - bu
cone arrestin - no
S-antigen - mouse
                                                                                                                                                                                                                                                                                                                                                                                                      beta-arrestin, bra
beta-arrestin1 - r
beta-arrestin 1, s
arrestin arr3L - b
arrestin - human (
arrestin isoform 1
beta-arrestin 2 -
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arrestin - fruit f
arrestin 1 - blueb
arrestin homolog -
arrestin homolog -
49K photoreceptor
arrestin 2 - blueb
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359 DSQADVEMFRQDTVHHQESVE 379

A; Titl: A; Titl: A; Refe A; Refe A; Refe A; Refe A; Rone A; Cross	30 31 31 32 32 32 33 33 33 33 33 33 33 33 33 33
A; Fittle: Arrestin-subypes in insect antennae. A; Reference number: A56607; MUID:9319955; PMID:8452755 A; Recession: B56607 A; Status; preliminary; nucleic acid sequence not shown; not compared with concept A; Status; preliminary; nucleic acid sequence not shown; not compared with concept A; Status; preliminary; nucleic acid sequence not shown; not compared with concept A; Status; preliminary; nucleic acid sequence not shown; not compared with concept A; Status; preliminary; nucleic acid sequence not shown; not compared with concept A; Status; preliminary; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept A; Status; nucleic acid sequence not shown; not compared with concept acid sequence not shown; not compared with concept acid sequence not shown; nucleic acid sequence not shown;	111.5 6.0 427 2 T23954 31 111.5 5.7 364 2 T26507 32 111.5 5.7 364 2 T26507 33 111.5 5.7 2413 2 S34670 34 111.5 5.6 344 2 T33421 35 110.5 5.6 344 2 T33421 36 110 5.6 456 2 T29948 37 107.5 5.4 460 2 T23955 39 106.5 5.4 460 2 T33420 40 106 5.4 347 2 S31144 40 106 5.4 347 2 S31144 41 102.5 5.2 464 2 T34538 42 102.5 5.1 1804 2 T34538 43 101.5 5.1 1804 2 T34538 44 100 5.1 359 2 B70534 45 99.5 5.0 600 2 S65788 ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS

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arrestin 1 - bluebottle fly (Calliphora vicina)
C;Species: Calliphora vicina
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C,Accession: A55081; S44291
G,Plangger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
Biol. Chem. 269, 26969-26975, 1994
A,Title: Mechanism of arrestin 2 function in rhabdomeric photoreceptors.
A,Reference number: A55081; MUID:95014564; PMID:7929436
                                                                                                                                                                             RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: FlyBase:Arr1
A;Cross-references: FlyBase:FBgn0000120
A;Introns: 36/3; 306/3; 349/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A;Acctus: preliminary A;Status: preliminary A;Nolecule type: mRNA A;Residues: 1-364 <HYD>
A;Residues: 1-364 <HYD>
A;Residues: GB:M30140; NID:G156961; PIDN:AAA28380.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Cross references: UNIPROT:P15372; GB:M30177
;Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vihtelic, T.S.; Benzer, S.
;Title: Twenty Drosophila visual system cDMA clones: one is a homolog of human arrestir, A34868
,NUID:90138926; PMID:2105491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arrestin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Residues: 1-364 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: A34867, A34868

Smith, D.P.; Shieh, B.H.; Zuker, C.S.
Title: Isolation and structure of an arrestin gene from Drosophila.
Accession: A34867

MUID: 90138925; PMID:1689056
                                                                                                                                                                                                                      357 EAEGSIE
                                                                                                                                                                                                                                           300 ALASTTLIASQDARDÁFGIÍVSVÁVKVKLFLGÁLGGELCÁELÞFILMHÞKÞSRKAQL---
                                                                                                                                                                                                                                                                                               240 VVLFQNGQFRNTIÁFMETSEGCÞLNÞGSSLÓKVMÝLVÞTLVANCDRAGÍÁVEGDÍKKKDT
                                                                                                                                                                                                                                                                                                              241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQ 300
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                                                                                                                                                                                                                                                           CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGBLSABLPFVLMHPKPGTKAKVİHA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVVNEKVEKKĆSENNMITLYMNRKDEVDSVTOVBEIDGIIVLDDEYVRONKKIEVOLVĆN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258;
                                                                                                                                                                                                                                                                                                                                                                 | QPCTLVRKDFMLSPGELBLEVTLDKQLYLHGERIGVNICIRNNSNKWYKKIKAMYQQGVD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MYYNEKVFKKCAPNGKVTLYMGKRDFYDHVSGVEBIDGIVVLDDEYIRDNRKVFGQIVCS
                                                                                                                                                                                                                                                                                                                                                ÓPĆTVVŔŔĎFLĹŚPĠĔĹĔĹĔVŤĹĎŔQĹŸHĤĠĔĸĬSVŇĬĆVŔŃŃĠŃŔVVŔŔĨŔĀŃŶŎŖĠŶĎ 239
                                                                                                                                                                                                                                                                                                                                                                                                                           PNAPSSVTLOQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQQQ
                                                                                                                                                                                                                                                                                                                                                                                                    PSSPAŚVVLĄČKASDESOPCĠVQYFVKIFTGDŚDCDRSHRRŚTINLĠIRKVŎYAPTKOĠI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PŔŶĠŔĖDĎĖMIĠĹŖŶŎĸĖĹŦĹVŚQQVCP-PQKQDIQLŤŔŊŎĖŔĹĹĸĸĹĠŚŇÁYPFVŊQMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRYGREEDEVMGINFOKELCLASEQIYPRPEKSDKEOTKLOERLLKKLGSNAIPFTFNIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.1%; Score 1384; DB 2; 70.3%; Pred. No. 1.1e-102; ative 51; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 364;
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                                                                                                                                                                                                                                                           R.Raning, K.; Freitag, J.; Krieger, J.; Breer, H. 6211. Signal. 5, 69-80, 1993
A;Title: Arrestin-subtypes in insect antennae. A;Reference number: A56607; MUID:93199955; PMID:8452755
A;Accession: A56607
                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                        A;Residues:
                                                                                                                                                                                                                                                                                                                                    arrestin homolog - migratory locust
C:Species: Locusta migratoria (migratory locust)
C:Date: 11-Aug-1995 #Sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                Matches
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 < PLA>
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                                                                                                                               Local 202;
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Best Local S
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73 ÉÉDÉVMÓLKETKEMVLÁKÉÓÍVÉQ-TKEKMÉLTPIÓÉRLMKKLGPNÁFFÉTÉHFPASSPS
                     66 EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
                                                                                         14
                                                                    1-407 <RAM>
                                                   ĸVŕĸĸſŦŔŊĠĸĊŤVŶĿĠĸŔĎŕĿĎĦĿĎĦŶĎŶĬĎĠĬŶŶŶĎŊĎŶĿŔ-ĠŖĸŶŕĠŎĿŦŦŦŶŔŶĠŔ
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                                                                                                                                 Conservative
                                                                                                                                            50.4%;
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126 SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQ-PCT 184

125 72 65 8 64;

Score 993.5; DB 2; Pred. No. 1.8e-71; 64; Mismatches 107;

__DB_2; Length 407; 107; Indels 15;

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A;Cross-references: UNIPROT:P51486; GB:X79072; NID:9483527; PIDN:CAA55672.1; PID
A;Note: the source is designated as Calliphora erythrocephala
355 -- QPEAET 360
                          361 DSQADVET 368
                                          301 CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGBLSAELPFVLMHPKPGTKAKVIHA 360
                                                                                                                                   180 ÓPCTVVRKDFLLSPÓBLELBVTLDRÓLYYHGEKÍSINÍCVRNNSNKVVKKÍKÁMVÓQGÍD 239
                                                                                                                                                                                                              121 PNAPSSVTLQQGEDDNGDPCGVSYYVKIPAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                          SLĀSTTĒLIASQEARDĀPĠIĪVŚYĀVKVKLPLGĀLGĠĒLCĀĒLPFILMHPKPSLKĀ-----
                                                                                                                                                                                                                                                                                                     1 MYVNÉKIEKKASENNMYTLYMNRŘEEVĎSVTQVEEVĎGÍVVLDDEVÍRONŘKIEVÔLIČN 60
                                                                                VVLÞÓNGGFRNTIAFAESSEGCELNEGSSLOKIMYLVENLAANCDRAGIÁVEGDVKHKNT
                                                                                                                                                                                                                                                                                                                          VVLFONGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLLSSNKORRGIALDGOIKRODQ 300
                                                                                                                                                        OPCTLVRKDFWLSPGELBLEVTLDKOLYLHGERIGVNICIRNNSNKMYKKIKAMVQOGVD 240
                                                                                                                                                                                        PSSPASÝVLÓQKANDSTQPĆĠÝQÝFÝKVFAĞENDCDŘSHŘŘŠŤÝNLGÍŘKVQYÁPŤKTGI 179
                                                                                                                                                                                                                                               PRYGREDDEMIGLRÞÓKELILVSOPVÝÞE-QKIDIOLÍKMÓERLLKKLGSNAYÞFILEMP 119
                                                                                                                                                                                                                                                                    FRYGREEDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                           67.7%; Score 1335; DB 2; 67.4%; Pred. No. 8.7e-99; tive 57; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                Length 363;
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arrestin

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59

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arrestin homolog - fruit fly (Drosophila miranda)
C;Species: Drosophila miranda
C;Species: Drosophila miranda
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: $11566
R;Krishnan, R.; Ganguly, R.
Nucleic Acids Res. 18, 5894, 1990
A;fitle: Nucleotide sequence of the arrestin-like 49 Kd protein gene of Drosophila mirar
A;Reference number: $11566; MUID:91016944; PMID:2216789
A;Accession: $11566
A;Status: preliminary; translation not shown
A;Residues: preliminary; translation not shown
A;Residues: 1401 cKRI>
A;Cross-references: UNIPROT:P19108; EMBL:X54084; NID:g7612; PIDN:CAA38019.1; PID:g295739
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 49.5%; Score 977.5; DB 2; Similarity 48.5%; Pred. No. 3.3e-70; 90; Conservative 76; Mismatches 113;
                                                        ---KAKVIHADSQADVETFRQDTIDQQASVDF 382
                                                                                                                         QCLASTTLLAQ-PDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT-----
                                                                                                                                                                                                                      DVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQD
                                                                                                                                                                                                                                                                                   Q-PCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVN1.CIRNNSNKMVKKIKAMVQQGV 239
                                                                                                                                                                                                                                                                                                                                                                     PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKI.QERLLKKLGSNAIPFTFNIS
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                                                                                                                                                                                                                                                              RLPSSLVSKGFTFSNGKISLEVTLDREIYYHGEKTAATVQVSNNSKKSVKSIKCFIVQHT 238
                                                                                                                                                                                                                                                                                                                                            PNSPSSVTLQQEGDDNGKPLGVEYTTRAFVGDSEDDRQHKRSMVSLVIKKLQYAPLNRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                            YRYGREEDEVMGVKFSKELILSRDEIVPM-TNPNMEMTPMQEKLVRKLGSNAHPFTFHFP
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                                                                                                  VNLASSTMVQEGKNTGDACGIVISYSVRIKLNCGTLGGEMQTDVPFKLLQPAPGTIEKKR
                                                                                                                                                                                EITMV-NAOFSKHVAOLETKEGCPITPGANLTKTFYLIPLAANNKDRHGIALDGHLKDED
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A;Title: A 49-kilodalton phosphoprotein in the Drosophila photoreceptor A;Reference number: A34856; MUID:90232360; PMID:2158671
A;Accession: A34856
                                                                                                                                                     arrestin 2 - bluebottle fly (Calliphora vicina)
c;Species: Calliphora vicina
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_
C;Accession: B55081; S44292
R;Plangger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
J. Biol. Chem. 269, 26969-26975, 1994
A;Title: Mechanism of arrestin 2 function in rhabdomeric A;Reference number: A55081; MUID:95014564; PMID:7929436
A;Accession: B55081
                                   A;Cross-references: UNIPROT:P51487; A;Note: the source is designated as C;Superfamily: arrestin
                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-401 <PLA>
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A;Cross-references: FlyBase:FBgn0000121
C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49K photoreceptor protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Spacie: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-401 < YAM>
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---KAKVIHADSQADVETFRQDTIDQQASVDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRYGREEDEVMGVKFSKELILCREQIVPM-TNPNMEMTPMQEKLVRKLGSSAHPFTFHFP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                            SNAMKKMKS I EQHRNVKGYYQDDDDDI VFEDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EITMV-NAQFSKHVAQLETKEGCPITPGANLTKTFYLIPLAANNKDRHGIALDGHLKDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNSPSSVTLOQEGDDNGKPLGVEYTIRAFVGDSEDDRQHKRSMVSLVIKKLQYAPLNRGQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVVSVKVFKKATPNGKVTFYLGRRDFIDHIDYCDPVDGVIVVEPDYLK-NRKVFGQLATT
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47.8%;
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; Pred. No. 4.7e-70;
74; Mismatches 115;
Score 942.5;
                                                        EMBL:X79073; NID:g483583; Calliphora erythrocephala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:M32141; NID:g158157; PIDN:AAA28833.1; PID:g158158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-Jul-1990 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382
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2
Length
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                                                                                                                                                                                                   photoreceptors
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                                                                               PIDN:CAA55673.1; PID:g48358
    401;
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357

297

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A. Status: nucleic acid sequence not shown
A. Molecule type: mRNA
A. Rolecule type: mRNA
A. Residues: 1-15, 'C', 17-30, 'L', 32, 'K', 34-83, 'Y', 85-176, 'K', 178-206, 'L', 208-333, 342-418
C. Comment: This protein is an arrestin homolog which acts analogously to desensitize the C. Superfamily: arrestin
C. Superfamily: arrestin
E;1-418/Product: beta-arrestin, brain #status predicted <MAT>
F;1-33,342-418/Product: beta-arrestin, lung #status predicted <MAZ>
                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-418 < LOH-
A; Residues: 1-418 < LOH-
A; Experimental source: brain
J. Biol. Chem. 268, 15640-15648, 1993
A; Title: Polypetide variants of beta-arrestin and arrestin3.
A; Reference number: A47140; MUID:93340166; PMID:8340388
A; A; Cession: JC2052
                                                                                                                            Ouery Match

Best Local Similarity 47.1%; Pred. No. 2.8e-64;
Matches 179; Conservative 76; Mismatches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
A34851
beta-arrestin, brain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Accession: A34851; JC2052 — revision 21-Oct-1992 #text_change 09-Jul-2004
R;Lohse, M.J.; Benovic, J.L.; Codina, J.; Caron, M.G.; Lefkowitz, R.J.
Science 248, 1547-1550, 1990
A;Title: Beta-arrestin: a protein that regulates beta-adrenergic receptor function.
A;Accession: A34851; MUID:90296080; PMID:2163110
                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: nucleic acid sequence not shown
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Matches 187; Conservative 70;
                 66 EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIDFTENISPNAPS 125
                                                                        EDLDVLÓLTFRKOLFVÁNVÓSFÉPAPEDKKPLTRLÓÉRLIKKLÓEHÁYFFTFEÍPPNIFC 125
                                                        RVPKKASPNGKLTVYLGKRDFVDHIDLVBPVDGVVLVDPEYLKE-RRVYVTLTCAFRYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 SNAMKKMKSIEQHRNTKGYYQDDDDNIVFEDF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 ---KAKVIHADSQADVETFRQDTIDQQASVDF 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 QCLASTTLLAQ-PDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT---- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 EITMV-NAQFSKHVÁQLÉTKÉGCÉTTÉGANLSKTFYLIÐLASNNKDRHGÍÁLDGHLKDED 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 DVVLFQNGSYRNTVASLETSEGCPIOPGSSLOKVMYLTPLLSSNKORRGIALDGOIKROD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 RLĖSSLVSKGFTFŚNĠKISLĖVTLDREIYYHĠGKVAATVQINNNSKKAVKNIKVFIIQHT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 Q-PCTLYRKDEMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMYKKIKAMVQQGV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 PNAPSSYTLOGGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTYTLGIRKIQFAPTKGGQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FRYGREEDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPETFNIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNÍASSTWVQDGKSTGĎÁCGIVÍSÝSVRIKÍNCGTÍGGEIQTDVÞFKÍLQÞAÞGSVEKKR 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MVVSVKVFKKATĖNGKVTFYLGRRHĖTDHFDYTDĖVDGVTVVDEDYLK-NRKVĖAQLATI
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70; Mismatches 122; Indels
                                                                                                                                                 DB 2; Length 418;
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A;Cross-references: UNIPROT:P29066; GB:M91589; NID:g949985; PIDN:AAA74459.1; PID:g203102
C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; not compared with conceptual translation A;Residues: 1-418 <ATT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K.Attramadal, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder A;Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin movel member of the arrestin/beta-arrestin gene family.

A;Reference number: A43404; MUID:92388146; PMID:1517224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 46.8
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta-arrestinl
364 EVPESETPVDTNLIELDTND 383
                               356 KVIHADSQADVETFRQDTID 375
                                       304 TLLREGANREILGIÍVSÝKVKVKLVVSRĞGLLĞDLASSDVAVELPFTLMHPKPKEEEPPHR 363
                                                                       306 TLLAQPDQRDAFGVIISYAVKVKLFL--GALGGELSA-----ELPFVLMHPKPGTK---A 355
                                                                                                             246 TAQÝKCFVÁMEÉADD--TVAÞSSTFCKVYTLTÞFLANNREKRGLÁLÞGKLKHEÐTNLÁSS 303
                                                                                                                                             246 NGSYRNTVASLETSEGCPIOPGSSLOKVMYLTPLLSSNKORRGIALDGQIKROPQCLAST 305
                                                                                                                                                                                186 TTRQĖLMSDKPLHLĖASLDKEI YYHGĖPISVNVHVTNNTNKTVKKI KISVROYADICLĖN 245
                                                                                                                                                                                                      186 VRKDFWLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQ 245
                                                                                                                                                                                                                                                      126 ŚVTLOPGPEDTGKAĆGVDYEVKAPCAENLEEKIHKKNSVRLVIKKVOVAPERPGPOPTAE 185
                                                                                                                                                                                                                                                                            126 SVTLQQGEDDNGDPCGVSYYVKIPAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                         66 EDIDVÍLGITERKOLFVÁNVÓSFÉPAPEDKKPLTRÍ OSKÍLKKLGEHÁYFÉTÉBÍ PÉNIFC 125
                                                                                                                                                                                                                                                                                                                                               66 EEDEVMGINFOKELCLASEQIYPRPEKSDKEOTKLOERLLKKLGSNAIPFTENISPNAPS 125
                                                                                                                                                                                                                                                                                                                                                                                                                 6 KVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEXIRDNRKVFGQIVCSFRYGR 65
                                                                                                                                                                                                                                                                                                                                                                                                 7 RVFKKASPNGKLTVYLGKRDFVDHIDLVDPVDGVVLVDPEYLKE-KRVYVTLTCAFRYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 EVPEHETPVDTNLIELDTND 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 TLLREGANREILGIÍVSÝKVKVKLVVSRĞGLLĞDLASSDVAVELPFTLMHPKPKEEPPHR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 TLLAQPDQRDAFGVIISYAVKVKLFL--GALGGELSA-----ELPFVLMHPKPGTK---A 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 TAQÝKCPVÁMEĖADD--TVAĖSŠTPCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 NGSYRNTVASLETSEGCPIOPGSSLOKVMYLTPLLSSNKORRGIALDGOIKRODOCLAST 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 TTRQFLMSDKPLHLEASLDKETYYHGEPISVNVHVTNNTNKTVKKIKISVRQYADICLEN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 VRKDFWLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMYKKIKAMVQQGVDVVLFQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 ŚVTLOPGPEDTGKAĆGVDYEVKAPCAENLEEKIHKKNSVRLVIKKVOYAPERPGPOPTAE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 SVTLQQGEDDNGDPCGVSYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.8%; Score 903.5; DB 2; Length 418; 46.8%; Pred. No. 2.8e-64; ative 78; Mismatches 111; Indels 13
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arrestin arr3L - bovine
N;Contains: arrestin arr3S
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Feb-1994 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004
C;Date: 16-Feb-1994 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47140; B47140; JC2051
R;Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Eodine, R.C.; Sanders, C.
J. Biol. Chem. 268, 15640-15648, 1993
A;Title: Polypeptide variants of beta-arrestin and arrestin3.
                                                                                                                                RESULT 11
A47140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:ARRB1; ARR1
A;Grose-references: GDB:141541; OMIM:107940
A;Map position: 11q13-11q13
C;Superfamily: arrestin
C;Keywords: alternative splicing
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A; Residues: 1-33,342-418 <PAR2>
A; Cross-references: GB:L04685; NID:g347956; PIDN:AAA35556.1;
A; Note: sequence extracted from NCBI backbone (NCBIP:134015)
C; Genetics:
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A;Title: Molecular analysis of human beta-arrestin-1: cloning, tissue distribula; Reference number: A46682; MUID:93252853; PMID:8486659
A;Accession: B46682
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C;Date: 22-Sep-1993 #text_change 09-Jul-2004
C;Accession: B46682; A46682
R;Parruti, G.; Peracchia, F.; Sallese, M.; Ambrosini, G.; Masini, M.; Rotil
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A;Status: not compared with conceptual translation
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beta-arrestin
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46.3%; Pred. No. 2.5e-63;
tive 78; Mismatches 113
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A; Description: Isolation o
A; Reference number: S18984
A; Accession: S18984
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A;Residues: 1-362,374-420 <5T2>
C;Comment: This protein plays a role in the regulation of
C;Superfamily: arrestin
F;1-420/Product: arrestin arr3L #status predicted <MAT>
F;1-362,374-420/Product: arrestin arr3S #status predicted
                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-409 <RAP>
A;Cross-references: UNIPROT:P32121; EMBL:Z11501; NID:g28850; PIDN:CAA77577.1; PID:g28851
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submitted to the EMBL Data Library, November 1991
A:Description: Isolation of a novel cDNA belonging
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A;Experimental source: brain
A;Note: sequence extracted from NCBI
A;Accession: B47140
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A; Residues: 1-420 <STE>
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                                                                                                                                                                                                                                                                                                                                                                                                                            ;Species: Homo sapiens (man)
;Date: 06-Jan-1995 #sequence_revision
;Accession: S18984
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es 167; Conserv
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                                     NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305
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Pred. No. 1.4e-62;
6; Mismatches 99;
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Pred. No. 5.8e-63;
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RESULT 14
A59279
beta-arrestin 2 - rat
C.Specise: Rattus norvegicus (Norway rat)
C.Date: 02-Jun-2000 #sequence revision 02-Jun-2000 #text_change /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 TAQÝKCPVÁQLEQDD--QVSÞSŠTFCKVYTTŤÞÍLSDNREKRGLÁLDGKLKHEÐTNÍLÁSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       RVĖKKSSĖNCKVTVYLGKRDĖVDĖLDQVDĖVDGVILVDEĖYLKO-RKVĖVTLTCAFRYGR
                                                                                                                                                                                                                                                                                                                                                                                                                     KVFKKCAPNGKVTLYMGKRDFVDHVSGVEFIDGIVVLDDEXIRDNRKVFGQIVCSFRYGR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 NGSYRNTVASLETSEGCPIOPGSSLOKVMYLTPLLSSNKORRGIALDGOIKRODQCLAST 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 TTPHÉLMŚDRSĹHĹĖASĹĎKEĽÝYHĊEPLNÝŇVHVTŃŃŚTKTÝKKĽKVSÝRQYAĎICĽÉS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVTLOGGEDDNGDECGVSYYVKIFAGESETDRTHRRSTVTLGIRKIOFAPTKOGOOPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.1%; Score 871; DB 2; Length 407;
44.3%; Pred. No. 1e-61;
tive 82; Mismatches 121; Indels :
                                            09-Jul-2004
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submitted to GenBank, August 1995
A;Reference number: A59279
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R;Braushum, the EMBL Data ....
submitted to the EMBL Data ....
A;Description: The sequence of
A;Reference number: Z21501
A;Accession: T34297
A;Status: preliminary; trans?
                                                                           RESULT 15
1734297
1794297
hypothetical protein F53H8.2 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C.Accession: 734297
C.Accession: 734297
C.Accession: 734297
                                                                    C; Pace.
C; Accession: T3429;
R; Bradshaw, H.; Gattung, S;
submitted to the EMBL Data Library, November 1995
The sequence of C: elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: I-320,'A',322-325,'A',327-330,'A',332-410 <AT2>A;Cross-references: GB:M91590; NID:g949986'
A;Note: sequence extracted from NCBL backbone (NCBIP:112790) A;Note: the sequence is revised in GenBank entry RATBARRES2, release for the sequence of the sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A,Residues: 295-410 <CRA>
A;Cross-references: EMBL:U03627; NID:g458202; PIDN:AAA17551.1; PID:g458203
C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Status: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: strain Sprague-Dawley; stage adult; tissue type brain; tissue 11b
I. Biol. Chem. 267, 1782-17890, 1992
A;Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin2 a novel member: A43404; MUID:92388146; PMID:1517224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Status: not compared with conceptual translation A/Residues: 1-410 <ATT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 TTLLAQPDQRDAPGVIISYAVKVKLFLGALGGELSAELPFVLMHPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 ONGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 TTRHFLMSDRRSLHLEASLDKELYYHGEPLNVNVHVTNNSAKTVKKIRVSVRQYADICLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 VRKDFMLSP-GELELEVTLDKOLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 ŚVTLOPÓPEDTGKAĆĠVDFEIRAFCAKŚIBEKSHKŔNSVRLIIRKVOFÁPETPGPOPSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 ERDEVMGLNFOKELCLASBQIYPRPEKSDKEOTKLOERLLKKLGSNAIPFTFNISPNAPS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch tch 44.1%; Score 869.5; DB 2 al Similarity 48.1%; Pred. No. 1.4e-61; 167; Conservative 76; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                      STIVKEGANKEVLGILVSYRVKVKLVV-SRGGDVSVELDFVLMHPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STAQÝKCPVÁQLÉQOD--QVSÞSŚTFCKVYTIŤÞÍLSDNREKRĞLÁLDĞÓLKHEDTNLÁS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDLDVÍJLSÉRKOLFIÁTYÓAFÉPMENPERPETRÍÓDRÍÍKKLGOHÁHÞFFFTÍPONLEC 126
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                                  from
                    GB/EMBL/DDBJ
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A;Residues: 1-454 <BRA>
A;Cross-references: EMBL:U41023; PIDN:AAA82342.1; CESP:F53H8.2
C;Genetics:
A;Gene: CESP:F53H8.2
A;Introns: 11/2; 61/1; 155/3; 189/2; 237/3; 290/2; 338/2; 389/3; 416/2
C;Superfamily: arrestin
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                                                                                                                  370
                                                                                       339 SAELPFVLMHPKP 351
                                                                                                                                                                               250 HIQNNSNKTVKKLKIYIIQVADICLFTTASYSCEVARIESNEGFFVGPGGTLSKVFAVCF
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                                                                                                                                                                                                                                          190 ALSNTVRLAIRKLTYAPPESRPQPMVDVSKYFMMSSGLLHMEVSLDKEMYYHGESISVNV
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                                                                                                                                                                                                                                                                                                                                     106 KKLGSNAIPFTFNISPNAPSSYTLQQGEDDNGDPCGVSYYVKIF-----AGESETDRT 158
                                                                                                                                                                                                                                                                                                         131 RKLGANAFPFWFEVAPKSASSVTLOPAPGDTGKPCGVDYELKTFVAVTDGSSGE-KPKKS 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                6 KVFKKCAPNGKVTLYMGKRDFVD------HVSGVEPID------GIVVLDDEY 46
                                                           FAELPETLTHSKP 382
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Result
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Maximum DB seq length: 2000000000
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 33222222222111111110
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1 MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQQASVDFE
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ARRA_CALVI
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Q6GU6
Q7QQV9
Q6GU6
Q7QSO8
Q9VJ33
ARRH_LIMPO
ARRB_DROMI
ARRB_DROMI
ARRB_CALVI
ARRH_LIMPO
Q86BWG
Q8MYB1
Q6HYB1
Q6HYB1
Q8MYB1
ARRI_RAT
ARRI_CAEEL
ARRZ_BOVIN
ARRI_HUMAN
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ARRZ_HUMAN
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Q7PMGS
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                                                                                                                                                                 o anopheles g
anopheles g
6 anopheles g
8 anopheles g
3 drosophila
2 locusta mig
7 drosophila
8 drosophila
7 calliphora
7 calliphora
1 imulus pol
6 halocynthia
1 ciona intes
8 xenopus lae
mus musculu
                                                                                                                                                                                                                                                                                                                                          3 anopheles g
5 anopheles g
9 ascalaphus
4 heliothis v
2 drosophila
6 calliphora
0 anopheles g
9 anopheles g
6 anopheles g
7 homo sapien
2 brachydanio
5 caenorhabdi
6 bos taurus
1 homo sapien
3 oryctolagus
4 xenopus lae
                                                                                                                      8 mus musculu
0 bos taurus
6 rattus norv
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61

FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120

Ş В Ş

181

В Ś 밁 Ş В Ś 뭕

361

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Name=ENSAGG0000010080;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                              61 FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTENIS 120
                                                                                                                                                                                                   35 MVYNEKVEKKCÁPNĠKVTĽYNĠKRĎEVĎHVSĠVĒĐĪĎĠĪVVĽĎĎĒŸĪRĎNŔKVEĠQĪVĊŚ
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                                                                             PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                                                                     PRÝGRÉEDÉVMGLNFOKELCLÁSEOÍ YFRPEKSDKEOTKLÓERLLKKLGSNÁTFFTFNÍS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 DŚQADVĖTĖRODTIDOQASVDĖE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA 360
                                                                                                                                                                                                                                                                                                                                                                       417 AA; 46591 MW; 4EE98A3C32257FCO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 VVLFQNGSYRNTVASLETSEGCFIQFGSSLQKVMYLTFLLSSNKQRRGIALDGQIKRQDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ČLASTTLLAQPDORDAPGVIÍSVAVKVKLFLGALGGBLSABLPFVLMHPKÞGTKAKVIHA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÓPCTĹVŔŔĎĖMĹŚPĠBĹĔĹĔŶŤĹĎŔQĹŶĹŀŀĠĔŔŤĠŶŇŤĊĨŔŇŃĠŇŔŇŶŔŔŤŔĂŃŶĠĊĠŶĎ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PŇĀĖŠŠVĪLOQGEDDNGDĖCGVŠYVYKIFĀGEŠĒĪDRĪHRRSTVĪLGIRKIOFĀPĪKOGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1973; DB 2; Length 417; 100.0%; Pred. No. 1.2e-144; tive 0; Mismatches 0; Indels 0
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Best Local Similarity
Matches 289; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    R GO; GO:0007600; P:sensory perception; IEA.
R GO; GO:0007165; P:sensory perception; IEA.
R InterPro; IPR0010598; Arrestin_C.
R InterPro; IPR011022; Arrestin_C.
IR InterPro; IRR011021; Arrestin_N.
Pfam; PF02752; Arrestin_N.
IR Pfam; PF02752; Arrestin_N.
IR Pfam; PF0339; Arrestin_N.
IR Pfam; PF0339; Arrestin_N.
IR Pfam; PF0339; Arrestin_N.
IR PROSITE; PF0339; ARRESTIN;
IR PROSITE; PF0339; ARRESTIN;
IR PROSITE; PF0329; ARRESTINS;
IR PROSITE; PS00295; ARRESTINS;
IR PROSITE; PS
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                                                         179
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Neuroptera, Ascalaphidae, Ascalaphus.
NCBI_TaxID=146496,
                                                                             119 PPNÁPATITLÓPGAEDOGEPCGYOYFLKAFYGESDTERPHARSSVSMOIRKÍOYÁPSKÓG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BIG9;
Q9BIG9;
01-JUN-2001
01-JUN-2001
01-MAR-2004
Arrest;
                                                                                                 120 SPNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A. ISSUE=Head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arrestin
                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                             RÓPĆTVÝRKDEMLSPODĽBĽBÝTĽDKOĽÝYĤĠEKŤAVNÍCÍRNNSNKVÝKKÍKÁMTÓOĠÝ
                                                                                                                                                    SPŘÝGŘÉDEVMGLNPRKDÍTÍVSEQIÝPSNĚK--VĚTŤKLÓDŘĹIKKLGPŇAÍPFKFVL 118
                                                                                                                                                                               395 DSQADVETFRODTIDOQASVDFE 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĊĹĀŚŢŢĹĹĀQĖĎQŔĎĀĖĠŸĨĬŚŸĀŸĸŸĸĹŦĹĠĀĹĠĠĔĹŚĀĔĹŖŦŸĹſĸĦŔĸĔĠŢĸĀĸŸĬĦĀ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVL ÞÓNGSÝRNTVASLETSEGCETÓÞGSSLOKVMYLTÞÍLLSSNKORRGTÁLÞGGTKRÓÞO 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÓÞĆTĽVŘKDÍMĽSÞÓBĽBĽBVŤĽDKOĽÝĽHGÉŘÍGVNÍĆÍRNNSNKMVKKÍKAMVQGGVĎ 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                           76.8%; Score 1515; DB 2; Length 3; 75.7%; Pred. No. 3.7e-109; tive 46; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Query Match Best Local S Matches 383

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Best Local S
Matches 277
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P55274;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heliothis virescens (Noctuid moth) (Owlet moth),
Eukaryota; Motazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis.
                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00309; ARRESTIN.
PRODOM; PD002099; ARRESTIN; 2.
PROSITE; PS00295; ARRESTINS; 1.
Sensory transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000698; Arrestin C. InterPro; IPR011022; Arrestin C. InterPro; IPR011021; Arrestin N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raming K., Freitag J., Krieger J., Bre "Arrestin-subtypes in insect antennae. Cell. Signal. 5:69-80(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: Belongs to the arrestin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arrestin homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence u
15-UUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSUE-Antenna;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B56607; B56607.
; P17870; 1G4M.
                          240
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PF02752; Arrestin_C; 1.
PF00339; Arrestin_N; 1.
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                                                                                                                                                                                                                                                                                                            277; Conserv
                                                                                                                                                                                                                                                      μ
                                                VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQ
                                                                                                QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMYKKIKAMVQQGVD
                                                                                                                                                       PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQCQ 180
                                                                                                                                                                                                                 FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS
                                                                                                                                                                                                                                                    MYZNEKVEKKCAPNGKITLYMAKRDEVDHISTVEPIDGVVLLDEEYVR-GRKVEGQMVCT
                                                                                                                                                                                                                                                                               MVYNEKVEKKCAPNGKVTLYMGKRDEVDHVSGVEPIDGJ VVLDDEYIRDNRKVEGQIVCS
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CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA
                                                                                  QPCTVVRKDFVLSPGQLELELTLDKQLYIHGETVAVNMCVRNHSNKVVKKIKACIQQGVD
                                                                                                                                         PGAPGSVILQPGLEDDGEPCGVQYYVKIFVGDSEIDRSHRRSTVALGIRKVQYAPAKPGP
                                                                                                                                                                                              FRYGREEDEVMGLNFYKELFLASEQIYPPPEKRNYELSRTQERLIKKLGDGAIPFRLTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVVLFONGOYRTTIAHLETQEGCPTQPGSALQKVMYLLPSLQSNKDRRGIALDGQIKRQD
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                           VVLFQNGQYRNIVASIETQDGCPLQPGSSLQKVLHL'fPTLAHNRDKRGIALDGQLKRSDT
                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                        76.0%; Score 1499; DB 1;
72.7%; Pred. No. 6.5e-108;
                                                                                                                                                                                                                                                                                                                                                                  42747 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update)
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                                                                                                                                                                                                                                                                                                                                                                    84BB92B1BB3DA573 CRC64;
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RESULT 5
      RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Leinker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA Goccye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Goccye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Goccye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Goccye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan L.X., RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Marid J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G., RA Marid J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Baraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Baraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Baraktaroglu L., Beasley E.M., RA Bartis M.C., Cawley S., Dahlke C., Davangort L.B., Davies P., Chandra I., RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I., RA Gorger S., Doughes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Doubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Harris N.L., Harrey D.A., Helman T.J., Hernandez J.R., Houck J., Harris N.L., Harrey D.A., Helman T.J., Wei M.-H., Ibegwam C., Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Harris N.L., Mattei B., McIntosh T.C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., RA Helson D.R., Nelson N., Nusskern D.R., Pacleb J.M., Ra McIntosh T., Karpen G.H., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Wobarry C., Morris J., Moshrefi A., Ra Merkulov G., Milshina N.V., Wobarry C., Morris J., Westee M.G., Ra Milsang N.C., Stapleton M., Skupski M.P., Smith T., Resee M.G., Pan S., Pollard J., Pari V., Reese M.G., Pan S., Pollard J., Pari V., Reese M.G., Pan
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P15372; Q9VJA8;
01-APR-1990 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Phosrestin II (Arrestin A) (Arrestin 1)
Name=Arri; Synonyms-Arra; ORFNames=CG5711;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90138926; PubMed=2105491;
Hyde D.R., Mecklenburg K.L., Pollock J.A., Vihtelic
"Twenty Drosophila visual system cDNA clones: one i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith D.P., Sheih B.-H., Zuker C.S.; "Isolation and structure of an arrestin gene from Drosophila."; Proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990).
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Yang .
Zhao
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Zheng X. Gibbs R. "The

Zhong W., Zhou X., Zhu S., Rubin G.M., Venter J.C.; Drosophila melanogaster.";

Zhu

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Smith H.O.,

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EMBL; M30177; ; NOT ANNOTATED CDS.

EMBL; M30140; AAA28380.1; -

EMBL; AE003657; AAF53644.1; -

EMBL; AY061824; AAL27635.1; -

PIR; A34867; A3
                                                                                   IntAct; P15372;
PlyBase; FBgn000
GO: 00005624;
GO: GO:0016028;
GO: GO:0016060;
InterPro; IPR000
                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=93303590; PubMed=8316831;
Dolph P.J., Rangamathan R., Colley N.J., H.
Zuker C.S., Rangamathan R., Colley N.J., H.
"Arrestin function in inactivation of G pr.
rhodopsin in vivo.";
Science 260:1910-1916(1993)
-1- FUNCTION: Regulates photogreceptor cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUNCTION: Regulates photoreceptor cell deactivation. Arr proteins are mediators of rhodopsin inactivation and are for the termination of the phototransduction cascade. Photoreceptors. Inner and outer segments, and the inner phosphorylated, but does not undergo light-induced
                                                      YBase; FBgn0000120; Arr1.
; GO:0005624; C:membrane fraction; IDA.
; GO:0016028; C:rhabdomere; IDA.
; GO:0016060; P:metarhodopsin inactivation;
:erPro; IPR000698; Arrestin_C.
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MEDLINE=91282780; PubMed=1905538;

Matsumoto H., Yamada T.;

"Phosrestins I and II: arrestin homologs which undergo differential light-induced phosphorylation in the Drosophila photoreceptor in
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STRAIN=Berkeley; TISSUB=Head;
MEDLINE=22426066; PubMed=12337569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Cha
George R.A., Guarin H., Kronmiller B., Pacleb J.M.,
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphorylation.
SIMILARITY: Belongs to the arrestin family.
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MEDLINE=22426069; PubMed=12537572;

Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Haxris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Annotation of the Drosophila melanogaster euchromatic genome: a Systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
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01-OCT-1996 (Rel. 34, Last sequence up
05-UUL-2004 (Rel. 44, Last annotation
Name=ARR1;
(Arrestin A) (Arrestin 1
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Best Local s
Matches 258
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Pfam; PF02752; Arrestin C; 1.
Pfam; PF00375; Arrestin N: 1.
PRINTS; PR0309; Arrestin N: 1.
PRODOM; PD002099; Arrestin; 2.
PROSITE; PS00209; Arrestin; 2.
PROSPHOTIATION; Sensory transduction; Vision.
SEQUENCE 364 AA; 40771 MM; ODCC764C4F890FC2 CRC64;
                                                                                                                                                                                                                                                                                   CALVI
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70.3%; Pred. No. 5.1e
vative 51; Mismatches
   moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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Best Local
SEQUENCE FROM N.A.

STRAIN-44RR, Yaounde, and L3-5;
STRAIN-44RR, Yaounde, and L3-5;
STRAIN-44RR, Yaounde, and L3-5;
Morlais I., Poncon N., Simard F., Cohuet A., Fonton M., Simard F., Cohuet A., Fonton M., Strain M., Fonton M., Simard F., Cohuet A., Fonton M., Simard F., Cohuet A., Fonton M., Simard F., Cohuet A., Fonton M., Font
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Pfam; PF00339; Arrestin_N; 1.
PRINTS; PR00309; ARRESTIN, 2.
PRODOm; PD002099; ARRESTINS; 1.
PROSITE; PS00295; ARRESTINS; 1.
Senbory transduction; Vision.
SEQUENCE 363 AA; 40680 MW; 70
                                                                                                                                                                                                                                                                                                                                                                                                              Q6VPPO PRELIMINARY; PRT; 245 AA.
Q6VPPO;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
Arrestin (Fragment).
                                                                                                                                                                                                                                                                                                                        Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Ano;
NCBI_TaxID=7165;
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HSSP; P17870; 1G4M.

InterPro; IPR001698; Arrestin.

InterPro; IPR011022; Arrestin C.

InterPro; IPR011021; Arrestin N.
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67.4%; Pred. No. 3.2e-95;
live 57; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7C345D818E46C23E CRC64;
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Matches
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InterPro; IPR011021; Arrestin_N
Pfam; PF02752; Arrestin_C; 1.
Pfam; PF00339; Arrestin_N; 1.
PRINTS; PR00309; ARRESTIN.
PRODOM; PD002099; Arrestin; 2.
NON_TER 1.
NON_TER 245 245
SEQUENCE 245 AA; 27038 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7Q2V9 PRELIMINARY; PRT; 431 AA.
Q7Q2V9;
Q1-MAR-2004 (TrEMBLrel. 26, Created)
Q1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 28, Last annotation update)
EbiP4989 (Kurtz arrestin-like protein ArrK) (Fragment).
EbiP4989 (Kurtz arrestin-like protein ArrK) (Fragment).
Name=ebiG4989; Synonyms=ARRK; ORFNames=ENSANGG00000003863;
Anopheles gamblae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anop
                 EMBL; BK000997; DAA00889.1; -.
HSSP; P17870; 1G4M.
GO; GO:0007500; P:sensory perception; 1
GO; GO:0007165; P:signal transduction;
InterPro; IPR000698; Arrestin.
                                                                                                                                                                                        Merrill C.E., Pitts R.J., Zwiebel L.J.; "Molecular characterization of arrestin
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles Genome Sequencing Submitted (MAR-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0007155; F:512
InterPro; IPR000698;
                                                                                                                                                                                                                                                                                                                                          MEDLINE=23159591; PubMed=14986925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=180454;
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les 245; Conserv
                                                                                                                                                               preliminary data.
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                                                                                                                                             AAAB01008966; EAA13078.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHADSQADVET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRODT 373
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IPR011022; Arrestin_C.
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27038 MW;
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Arrestin_N.
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; Pred. No. 3.7e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Consortium;
EMBL/GenBank/DDBJ databases
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Q66GUG
D1 O66GI
D1 O66GI
D1 O66GI
D1 25-00
D1 25-00
D2 Arroyl
OC Bukane
OC Neop
OC Neo
                                  AX MEDIINE=331;9591; PubMed=14986925;
RA Merrill C.E., Pitts R.J., Zwiebel L.J.;
RT "Molecular characterization of arrestin family members in the malaria rector mosquito, Anopheles gambiae.";
RI Insect Mol. Biol. 12:641-650(2003).";
RI Interpro; IPR0100698 1;
DR Interpro; IPR01102; Arrestin C.
DR Interpro; IPR01102; Arrestin C.
DR Ffam; PF02752; Arrestin N.; 1.
DR PF0339; Arrestin N; 1.
DR PF0339; Arrestin N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR PRINTS; PR00309; ARRESTIN.
DR PROSTE; PS00209; ARRESTIN.
DR PROSTE; PS00209; ARRESTIN.; 1.
SQ SEQUENCE 398 AA, 44536 MW; 73DD73FB34F01418 CRC64;
                                       Query Match
Best Local S
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25-OCT-2004 (TrEMBLrel. 28, Crevel-25-OCT-2004 (TrEMBLrel. 28, Lasues-CT-2004 (TrEMBLrel. 28, Lasues-CT-2004 (TrEMBLrel. 28, Lasues-CT-2004)
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Eukaryota; Metazoa; Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=PEST;
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Best Local Similarity
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Pfam; PP02752; Arrestin C; 1.
Pfam; PP00339; Arrestin N; 1.
PRINTS; PR00309; ARRESTIN; 1.
PRODOM; PD002099; Arrestin; 2.
PROSITE; P800295; ARRESTINS; 1.
NON TER
NON_TER
SEQUENCE 431 AA; 47810 MW; 850
                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 TLLAQPDQRDAPGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSKEYTĹKÞNKTHLÉASĹĎKEĹÝHĤĠĖSLSVNVHÍANNŚSKTVKKÍKVSVRÓFAĎICĹFS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMVKKIKAMVOQGVDVVLFO 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVTLOOGEDDNGDPCGVSYVVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDLDÝLĠĹTFRKDĹYĹÁŚĖĠÍÝÞ-ÞLETĎRPLÍRĽĢĖŔĹIRKĽĠANÀYÞFYFEVPÞHCÞA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEDEVMGINFOKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTENISPNAPS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVFKKSSSNGKITVYLGKRDFVDHITHVDFIDGVVLIDFDYVKE-RKVFGHVLAAFRYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 431
431 AA; 47810 MW; 85C110785A815916 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
51.8%; Score 1023; DB 2; 52.3%; Pred. No. 5.9e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.5%; Score 1036; DB 2; Length 4:
54.1%; Pred. No. 6.5e-72;
tive 75; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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               Length
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QCSOB
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Best Local S
                                                                                                                                                                                                   Matches 204;
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HSSP; P17870; 1G4M.

GO; GO:0007600; P:sensory perception; IEA.
InterPro; IPR000698; Arrestin.
InterPro; IPR01102; Arrestin.
InterPro; IPR011021; Arrestin.
InterPro; IPR011021; Arrestin.
Pfam; PF02752; Arrestin.C: 1...
Pfam; PF02752; Arrestin.C: 1...
Pfam; PF02339; Arrestin.C: 1...
Pfam; PF00339; Arrestin.C: 1...
PRODOM; PF00399; Arrestin.C: 1...
PRODOM; PF00299; Arrestin.C: 1...
PRODOM; PF00299; Arrestin. 2...
PROSITE; PS00295; ARRESTINS; 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-I-CAUTION: The sequence shown here is derived from an Preliminary data.

Preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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1 MVYNFKVEKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS 60
                                                                                                                                                                           Similarity 52.3
04; Conservative
                                                                                                                                                                                                                                                                               401 AA; 44862 MW; F307885989AC4EE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 VIHADSQADVETFRQDT---IPQQASVDFE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 QCLASTTLLAQPD-QRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT--KAK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 EVTMV-NAQESKHIÁSLÉTRÉGCÉTTÉGASETKSFELVÉLASSNKDRRGTÁLDGHLKEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 SMÁÞŚSÝTLÓAĞEDĎTĠKÞLĠVEYAIKAHVĠĒDĒSĎKGHKŔŚAŸTLTÍKKLÓYÁÞVSRĠR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PMAPSSVTLQOGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YŔÝĠŔĖĖĎĖVMĠVKĖSKĖMVĹTKĖQĬŶĖM-ĒNANMĖMŤŖMĊĖŔĹVKKĹĠANĀFĖĖŤĖHFP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNALKKMKSIERHRYENSHYADDDDNIVFE 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVVAVKVĖKKSAPNGKLTVYLGKRDĖTDHTDYCDPIDGVIVLDEBYLR-GRKVĖGQLITT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVINEKVEKKCAPNGKVTLYMGKRDEVDHVSGVBPIDGIVVLDDEVIRDNRKVEGQIVCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRYGREEDEWMGLNFOKELCLASEQIYPRPEKSDKEQTKLOERLLKKLGSNAIPFTFNIS 120
                                                                                                                                                                                                           51.8%;
                                                                                                                                                                   65;
                                                                                                           Score 1023; DB 2; Length 401;
Pred. No. 6e-71;
65; Mismatches 111; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
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RA Adams M.D., Celniker S.E., Li P.W., Kyans C.A., Godayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Expandell M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Pandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Pandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Pelt G., Nelson C.R., Gabor G.L.,
RA Barandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Barandon R.M., Bastler E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ghoshos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gloden K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieva S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,
RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Renington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9V393;
Q9V393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Musccmorpha;

Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CG1487-PA (Kurtz arrestin) (LD31082p).
Nameskrz; ORFNames=CG1487;
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           MEDLINE-22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Kaminker J.S., Bergman C.M., Kronmiller
Patel S., Frise E., Wheeler D.A., Lewis
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MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronm
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Ashburner M., Celniker S.
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enome Biol. 3:RESEARCH0084-RESEARCH0084(2002)
                                                                                                                                                       ye M., Chavez ..., Guaringe R., Gonzalez M., Guaringe R., Mungall C.J., Nunda A., Mungall C.J., Nunda A., Mungall C.J., W
                                                                        AE003780;
AF221066;
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P17870; 1G4M.
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AAF32365.1;
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Dorsett V., Dresnek D., Far
C., Guarin H., Krommiller B.,
J., Nunco J., Pacleb J., Pa
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S.E., Rubin
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r B., Li P., L
r, Paragas V., Paragas V.,
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collabbetween the Swiss Institute of Bioinformatics and the EMBI outst. the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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TISSUE=Antenna;
MEDLINE=9319955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;
Raming K., Freitag J., Krieger J., Breer H.;
"Arrestin-subtypes in insect antennae.";
Cell. Signal. 5:69-80(1993).
-i-SIMILARITY: Belongs to the arrestin family.
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01-OCT-1939 (Rel. 3
15-JUL-1999 (Rel. 3
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Eukaryota; Metazoa; Arthropoda; Hexapoda; In
Neopteara; Orthopteroidea; Orthoptera; Caelif
Acridoidea; Acrididae; Oedipodinae; Locusta.
111
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MEDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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MEDLINE=90232360; PubMed=2158671;
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtls K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dew I., Diew I., Diesvam C.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Goor F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McIntosh T.C., Siden N.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shice B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Mang Z.-Y., Wassarman D.A., Weinston M., Skupski M.P., Smith T.,
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RA Yell-K., Wassarman D.A., Weinstock G.M., Weinschbach J.,
RA Yell-K., Wassarman D.A., Morley K.C., Wu D., Yang S., Zhou Y., Zhong W., Smith H.O.,
RA Yell-K., W
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Sutton G.G., W
Brandon R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science
                                                                                                                                                                                     MEDLINE-94242441; PubMed=8185954; DOI=10.1016/0896-6273(94)90309-3; Matsumoto H., Kurien B.T., Takagi Y., Kahn E.S., Kinumi T., Komori I Yamada T., Hayashi F., Isono K., Pak W.L.; "Phogrestin I undergoes the earliest light-induced phosphorylation B. Calcium/calmodulin-dependent protein kinase in Drosophila
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                                                                                                                                              photoreceptors.";
Neuron 12:997-1010(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                            Matsumoto H., Yamada T.; "Phosrestins I and II: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91282780;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lewis S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Annotation of the Drosophila melanogaster
               plexiform regions of the retina.
PTM: Phosphorylated upon light exposure.
SIMILARITY: Belongs to the arrestin family.
                                                      transduction.
TISSUE SPECIFICITY: Inner and plexiform regions of the retir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.A., Lewis S.
3.G., Wortman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             review.
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Reese M.G.,
chen H.,
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Ketchum K.A.,
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ARRB AC DT DT DT GN

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1 01-NOV-1990 (Rel. 16, Created)

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JT 01-NOV-1990 (Rel. 44, Last annotation update)

DE phosrestin I (Arrestin B) (Arrestin 2) (49 kf

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SEQUENCE
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MOD_RES 366
VARIANT 109
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EMBL; AE003554; AAF50380.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD002099; Arrestin; 2. PROSITE; PS00295; ARRESTINS; 1.
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InterPro; IPR011022; Arrestin_C.
InterPro; IPR011021; Arrestin_N.
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GO; GO:0016028; C:rhabdomere; IDA.
GO; GO:0005625; C:soluble fraction; IDA.
GO; GO:0015060; P:metarhodopsin inactivation;
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HSSP; P17870; 1G4M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0000121; Arr2.
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                                                        VNLASSTMVQEGKSTGDACGIVISYSVRIKLNCGTLGGEMQTDVPFKLLQPAPGTIEKKR
                                                                               QCLASTTLLAQ-PDQRDAFGVI;SYAVKVKLFLGALGGELSAELPFVLMHPKPGT-----
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                                                                                                                                                                                                                                               PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRK1QFAPTKQGQ
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SNAMKKMKSIEQHRNVKGYYQDDDDNIVFEDF
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R Types; FBG0001255; Dmir\Arr2.

InterPro; IPR000698; Arrestin. C.
R InterPro; IPR011021; Arrestin. C.
R InterPro; IPR011021; Arrestin. N.
Pfam; PF02752; Arrestin. C.
R Pfam; PF0339; Arrestin. N.
R Pfam; PF0339; Arrestin. N.
R PFNUTS; PF00309; Arrestin. N.
R PFNDDOm; PF00209; Arrestin. 2.
R PROSITE; P500209; ARRESTINS; I.
R PROSITE; P500209; ARRESTINS; I.
R PROSITE; P500209; ARRESTINS; I.
R PHOSPHORY Jation; Sensory transduction; Vision.
Q SEQUENCE 401 AA; 45014 MW; E46EEBC2485AF99C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license agreement (See http://www.isb-sib.ch/announce.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P17870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
358 SNAMKKMKSIEQHRNVKGYYQDDDDNIVFEDF
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"Nucleotide sequence of the arrestin-like 49 Kd protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91016944; PubMed=2216789;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                              300 QCLASTTLLAQ-PDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT-----
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                         ---KAKVIHADSQADVETFRODTIDQQASVDF
                                           VNÍASSÍMVQEGKNTGBÁCGIVÍSÝSVRIKÍNCGTÍGGÉMQTDVÉFKLIQFAÉGTIEKKR 357
                                                                                                                           DVVLFQNGSYRNTVASLETSEGCÞIQÞGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQD
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48.5%; Pred. No. 2e-67;
tive 76; Mismatches 113; Indels
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Best Local S
Matches 186
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PRODOM, PD002099, Arrestin, 2.
PROSITE, PS00295, ARRESTING, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000698; Arrestin.
InterPro; IPR011022; Arrestin_C.
InterPro; IPR011021; Arrestin_N.
Pfam; PF02752; Arrestin_C; 1.
Pfam; PF02339; Arrestin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PIR; B55081; B55081.
HSSP; P17870; 1G4M.
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Plangger A., Malicki D., Whitney M., Paulsen R.;
Plangger A. Malicki D., Whitney M., Paulsen R.;
"Mechanism of arrestin 2 function in rhabdomeric photoreceptors.
J. Biol. Chem. 269:26969-26975 (1994).
-!- FUNCTION: Directly interacts with light-activated rhodopsin.
the dephosphorylation of metarhodopsin. Interacts the dephosphorylation of metarhodopsin. Interacts of the arrestin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      irect protein sequencing; Phosphorylation; Sensory transduction;
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P51487;
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Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Calliphora.
NCBI_TaxID=7373;
241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQ
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(Rel. 34, Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.5%; Score 937.5; DB 1
47.6%; Pred. No. 2.6e-64;
tive 70; Mismatches 122
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rhabdomeric photoreceptors.
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Result
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is derived by analysis of the total score distribution.
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Maximum Match 100%
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       AAG67781
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ABG69495
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ADQ89588
ABR84484
ABB58174
ABB61964
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ABR84476
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Compugen Ltd
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Abr84476 Mosquito
Abb61736 Drosophil
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4 Mosquito
4 Drosophil
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9 Amino aci
8 Amino aci
Rat Prote
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173	351.5	361.5	482.5	497.5	497.5	516.5	516.5	516.5	516.5	661	761	761	779.5	780	780.5	865	869.5	869.5	869.5
8.8	17.8	18.3	24.5	25.2	25.2	26.2	26.2	26.2	26.2	33.5	38.6	38.6	39.5	39.5	39.6	43.8			44.1
65	456	212	182	315	180	187	187	182	182	468	405	405	388	405	388	454	526	526	526
4	4	4	7	σ	σ	7	σ	7	7	4	œ	8	4	4	4	8	8	œ	8
ABB42223	ABB58949	AAG73899	ADD27197	ADA00636	ADA00634	ADD27507	ABU70623	ADD27127	ADD27419	AAM79747	ADR41708	ADQ14327	AAG67782	AAM78763	AAG67783	ADN24049	ADR23186	ADR23188	ADR23187
Abb42223	Abb58949	Aag73899	Add27197	Ada00636	Ada00634	Add27507	Abu70623	Add27127	Add27419	Aam79747	Adr41708	Adq14327	Aag67782	Aam78763	Aag67783	Adn24049	Adr23186	Adr23188	Adr23187
_	_	_	7 Human	6 Human	4 Human	7 Human	3 Human	7 Human adi	9 Human	7 Human	8 Protein 8	7 Human	2 Amino		3 Amino	9 Bacterial		8 Green	7 Yellow

ALIGNMENTS

RESULT 1 ABP52833 ID P52833 nopheles gambiae; odourant receptor; 26-JAN-2001; 24-JAN-2002; Anopheles gambiae arrestin 1 01-NOV-2002 (first entry) ABP52833; ABP52833 standard; protein; Zwiebel LJ; 28-JAN-2002; 2002WO-US002549 01-AUG-2002. WO200259274-A2. Anopheles gambiae. (UYVA-) UNIV VANDERBILT. 2001US-0264649P. 2002US-00056405. mosquito; olfactory gene; arrestin 1; pest control; olfaction. 383 protein SEQ ID ጅ NO: 2

The present invention describes a purified Anopheles gambiae olfaction polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively modified amino acid sequence of them, or a sequence of (S1) with at least 20 consecutive residues. Also described: (1) an isolated polynucleotide comprising: (a) a nucleotide sequence encoding the purified Anopheles gambiae olfaction polypeptide; or (b) a nucleotide sequence that hybridises under stringent conditions to a hybridisation probe comprising a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence (see AB075102 to AB075105 and AB075110 to AB075113) (S2), or its complement; and (2) a method for identifying an agent that binds to

New mosquito olfaction polypeptides and polynucleotides, useful for mosquito management, i.e. controlling the pest and disease vectors, for identifying pest control agents.

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Claim 18; Fig 2; 96pp; English.

WPI; 2002-627421/67. N-PSDB; ABQ75102.

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RESULT 2
ABR94476
ID ABR9
ACC ABR9
ACC ABR9
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                                                                                                                                                                                                   WO2003076590-A2.
                                                                                                                                                                                                                                       Anopheles gambiae.
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Drosophila melanogaster.
          Drosophila, developmental biology; cell signalling; insecticide; pharmaceutical.
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N-PSDB; ACF79716.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
   ADQ89588;
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to
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DB; ABL05839.
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                                                                                                                                                                                                                                                     VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQ 300
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                                                                                                                                                                                                                                                                                                                                                                                   PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                         FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEFIDGIVVLDDEYIRDNRKVFGQIVCS
                                                                                                                                       DSQADVE
                                                                                                                                                                        ALASTTLIASQDARDAFGIIVSYAVKVKLFLGALGGELCAELPFILMHPKPSRKAQL---
                                                                                                                                                                                           CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVVNFKVFKKCSPNNMITLYMNRRDFVDSVTQVEPIDGIIVLIDDEYVRQNRKIFVQLVCN
                                                                                                             EAEGSIE
                                                                                                                                                                                                                                   VVLFQNGQFRNTIAFMETSEGCPLNPGSSLQKVMYLVPTLVANCDRAGIAVEGDIKRKDT
                                                                                                                                                                                                                                                                                                 QPCTVVRKDFLLSPGELELEVTLDKQLYHHGEKISVNICVRNNSNKVVKKIKAMVQQGVD
                                                                                                                                                                                                                                                                                                                                                             PSSPASVVLQQKASDESQPCGVQYFVKIFTGDSDCDRSHRRSTINLGIRKVQYAPTKQGI
                                                                                                                                                                                                                                                                                                                                                                                                                         FRYGREDDEMIGERFOKELTEVSQQVCP-PQKQDIQLTKMQERLEKKEGSNAYPFVMQMP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences
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2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1384; DB 4;
Pred. No. 1.5e-135;
1; Mismatches 54;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a polynucleotide for preventing, treating or diagnosing a disease in an individual. The composition or the polypeptide, polynucleotide or RNA precursor, or antibody is useful for diagnosing, preventing or treating diseases (e.g. cell proliferative diseases such as cancer) in an individual. These may also be used for identifying substances capable of binding to or modulating the function of the polypeptide, capable of affecting the function of the corresponding gene, or capable of inhibiting the cell division cycle or cell cycle progression, preferably mitosis and/or meiosis. The present sequence represents an antagonist of cell cycle progression protein
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cell cycle progression genes and proteins for modulating cell cycle progression in cells, for preventing, treating or diagnosing cell proliferative diseases (e.g. cancer) or for identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-2003; 2003US-0439123P
06-MAY-2003; 2003US-0468402P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitosis or meiosis.
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                                                                                                                                         181
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                                                                                                                                                                                                                                                                  61
 CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA
                                                                                                                                                                                                                                                                                                               MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
                                                                  VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQ
                                                                                                                            QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVD
                                                                                                                                                                        PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                                                                                                                                                                                                    FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120
                                                                                                                                                                                                                                                                                                 MVVNFKVFKKCSPNNMITLYMNRRDFVDSVTQVEPIDGIIVLDDEYVRQNRKIFVQLVCN
                                                                                                                                                                                                                                                                                                                                                                                                                          364 AA;
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                                                VVLFQNGQFRNTIAFMETSEGCPLNPGSSLQKVMYLVPTLVANCDRAGIAVEGDIKRKDT
                                                                                                            QPCTVVRKDFLLSPGELELEVTLDKQLYHHGEKISVNICVRNNSNKVVKKIKAMVQQGVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; cell division cycle; mitosis; meiosis;
                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                                           Score 1384; DB 8;
Pred. No. 1.5e-135;
1; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
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                                                                                                                                                                                                                                                                                                                                                                                          Length 364;
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The present sequence is the protein sequence of arrestin 2, a novel comparity olfaction molecule. The invention provides 9 novel mosquito and odorant receptor molecules 1-7. The odorant receptor molecules 1-7. The odorant receptors function comparity of a ligand-induced signal transduction pathway for the activation of the molecules 1-7. The odorant receptors function of and arrestin as an 'off; switch for the odorant receptors act as an 'on' switch compounds that modulate arrestin 2 dentifying compounds that interfere compounds that modulate arrestin 2 activity. These are useful for the control of mosquitoes, particularly by reducing their ability to locate the outcase of bloodmeal.
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Fig 12b; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mosquito arrestin 1 and 2 genes and polypeptides, useful for identifying mosquito olfaction molecule binding compounds which reduce the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYVA-) UNIV VANDERBILT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAR-2003; 2003WO-US007174.
                       60 YRYGREEDEVNGVKESKEMYTTKEGIYEM-ENAMMEMTEMQERLVKKLGANAFFFTFHFF 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arrestin 2; mosquito; olfaction; insecticide; antimalarial.
                                                                                                1 MYYNFKVFKKCAPNGKYTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mosquito olfaction molecule,
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                                               FRYGREEDEVMGLNFOKELCLASEQIYPRPEKSDKBQTKLQERLLKKLGSNAIPFTFNIS 120
                                                                                MVVAVKVĖKKSAPNGKLTVYLIGKRDĖ IDHTDYCDĖ IDGVIVLDEBYLR-GRKVĖGQLITT
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)B; ACF79731.
                                                                                                                                                                 Conservative
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                                                                                                                                                   51.8%; Score 1023; DB 7; 52.3%; Pred. No. 1.2e-97; tive 65; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Encoded by AG"
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                                                                       Query Match
                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention insecticides interactions in higher eukaryotes for the development of discloses genomic DNA sequences (ABL01840-ABL16175) and pharmaceutical drugs. The invention sequences (ABL01840-ABL16175) and the encoded proteins (appressed DNA BP27072). The sequence data for this patent did not form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences (ABB73737-from WIPO at ftp.wipo.int/pub/published_pct_sequences format directly
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ABB58174
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                                                                                                                                                                                      Disclosure; SEQ ID NO 1314; 21pp + Sequence Listing; English.
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genes from Drosophila
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 1314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB58174;
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                                                                                                                                                                                                                                                                                                               2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 VNALKKMKSIERHRYENSHYADDDDNIVFE 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 VNÍASSTÍLISEGKCPSDÁMGIVÍSÝSLRVKÍNCGTÍGGELQTDVÞFKLMNÞAÞGSVERER 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 QCLASTTLLAQPD-QRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT--KAK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 EVTMV-NAQPSKHIASLÉTREGCETTEGASETKSFELVELASSNKORRGTALDGHLKEDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 smápssvítí (adgebbí tigkelg vevalkahv gébés bkohkrásav títtikktóvá evsrór 178
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and coll-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57377-ABB72072). The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                            New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                   23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB61964 standard;
                                                                                              Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                             WO200171042-A2
                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                               (PEKE ) PE
                                                                                                                                                            2001-656860/75.
DB; ABL06067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSKEFMMKPNKIHLEATLDKELYHHGEKISVNVHVANNSNRTVKKIKVCVRQFADICLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQ 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVSLQPAPGDVGKSCGVDYELKAFVGENVEDKPHKRNSVRLTIRKVMYAPSKVGEQPSIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLITNPAQRESLGIMVHYKVKVKLLISSPLLNGDLVAELPFTLMHPKP
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2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
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                                                                                             12684; 21pp + Sequence Listing; English
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                                                                                                                                                                                          PWD,
                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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0; Mismatches 87;
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             Berstein
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                                                                                                                                                                                                                                                                                                                                           AAG67780
                                                     03-MAR-2000; 2000US-0186706P
                                                                         05-MAR-2001; 2001WO-US007304
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                             Amino acid
                                                                                               13-SEP-2001.
                                                                                                                   WO200167106-A2
                                                                                                                                                 Region
                                  (MILL-) MILLENNUM PHARM INC.
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SSXSS
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from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  PNAPSSYTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEFIDGIVVLDDEYIRDNRKVFGQIVCS
                                                                                             VNLASSTMVQEGKSTGDACGIVISYSVRIKLNCGTLGGEMQTDVPFKLLQPAPGTIEKKR
                                                                                                                                                                                                                                            DVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQD 299
                                                                                                                                                                                                                                                                                                                                          Q-PCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKWVKKIKAMVQQGV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRYGREEDEVMGVKFSKELILCREQIVPM-TNPNMEMTPMQEKLVRKLGSNAYPFTFHFP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120
SNAMKKMKSIEQHRNVKGYYQDDDDNIVFEDF
                                           ---KAKVIHADSQADVETFRODTIDQQASVDF 382
                                                                                                                                           QCLASTTLLAQ-PDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT-----
                                                                                                                                                                                           EITMV-NAQFSKHVAQLETKEGCPITPGANLTKTFYLIPLAANNKDRHGIALDGHLKDED
                                                                                                                                                                                                                                                                                            RLPSSLVSKGFTFSNGKISLEVTLDREIYYHGEKTAATVQVSNNSKKSVKSIKCFIVOHT
                                                                                                                                                                                                                                                                                                                                                                                          PNSPSSVTLQQEGDDNGKPLGVEYTIRAFVGDSEDDRQHKRSMVSLVIKKLQYAPLNRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVVSVKVFKKATPNGKVTFYLGRRDFIDHIDYCDPVDGVIVVEPDYLK-NRKVFGQLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 2.1e-93;
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AAG67780 standard; protein; 410 AA.

AAG67780;

10-DEC-2001 (first entry)

Amino acid sequence of human beta-arrestin 1B.

Arrestin; phosphorylation-independent arrestin mutant;
G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa; stationary night blindness; colour blindness; nephrogenic DI; isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma; familial hypocalciuric hypercalcemia; hyperparathyroidism; neurological disorder.

Homo sapiens.

Key

Location/Qualifiers

Region

155. .184

/note= "putative phosphorylation-recognition region"
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2001-602637/68

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RESULT 9
AAG67778
ID AAG6
XX
AC AAG6
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AC AAG6
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AC AAG6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents an arrestin protein. The specification describes phosphorylation-independent arrestin mutants. These mutants are content of the sequence of the comprises contacting assays to identify ligands and/or modulators of G CC constitutively active arrestin mutant with a test compound; and a GCC constitutively active arrestin mutant with a test compound; and a contential ligand the ability of the test compound to modulate binding of CC the test compound is a GPCR ligand. The method is used for identifying a GPCR ligand. The method is used for identifying CC treating patients having e.g. retinitis pigmentosa, stationary night contents, hyperfunctioning thyroid adenomas, familial hypocalciuric for uses as human therapeutics. Modulators of GPCR may be used for CC deficiency, hyperfunctioning thyroid adenomas, stationary night contents, the content of the sequence of the compound to hypercalcemia, hyperparathyroidism and neurological disorders. The methods may be used for screening pluralities of test compounds (e.g. a CC identification of natural and surrogate agonists of orphan GPCRs, and for CC identification of GPCR antagonists and/or agonists
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                                                              AAG67778 standard;
                                        AAG67778;
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Best Local
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                                                                                                                                                             363 QADVETFRODTID 375
                                                                                                                                                                                                   304
                                                                                                                                                                                                                             246 TAQYKCPVAMEEADD--TVAÞSSTFCKVYTLTÞFLANNREKRGLALDGKLKHEDTNLÁSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for in
                                                                                                                                                                                                                                                                                                       126 ŚVTĹQPĠPEDTĠKAĊĠVDYEVKAFCAĖNLEEKIHKRNSVRĹVÍRKVQYĀPERPĠPQPTAE
                                                                                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176;
                                                                                                                                  PVDTNLIELDTND 375
                                                                                                                                                                                          TLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTK---AKVIHADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLLREGANREILGIÍVSYKVKVKL-VESRÓGDVAVÉLÞFTLMÍÞKÞKEEFPHREVÞENET
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                                                                                                                                                                                                                                            NGSYRNTVASLETSEGCDIQPGSSLQKVMYLTELLSSNKQRRGIALDGQIKRQDQCLAST 305
                                                                                                                                                                                                                                                                                     TTRQFLMSDKPĹHĹĖASĹĎKEI YYHĠEPÍSÝNVHVTŇŇTŃKTÝKKÍ KISVRQYAĎICĹÉN
                                                                                                                                                                                                                                                                                                                                                                      SVTLQQGEDDNGDPCGV8YYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                      <u> BDLDVLĠĹTĖRKDĹFVÁNVQSFÞPAPEDKKPLŤRĹQĖRĹĹKKĹĠEHÁYÞFŤFBÍPÞNLÞC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                               EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                         Protein; 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.0%;
47.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 907.5; DB 4
Pred. No. 1.5e-85;
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                                                                                                                                      Query Match
Best Local (
                                                                                                     Matches 179;
                                                                                                                                                                                                                                                                                                                     Identifying a G protein-coupled receptor ligand, useful for treating retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for vitro screening assays.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-602637/68
126 SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                03-MAR-2000; 2000US-0186706P.
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                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arrestin; phosphorylation-independent arrestin mutant; G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigm stationary night blindness; colour blindness; nephrogenic DI; isolated glucocorticoid deficiency; hyperfunctioning thyroid familial hypocalciuric hypercalcemia; hyperparathyroidism; neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of bovine beta-arrestin 1A.
                                                      EDLDVLGĹTFRKDĹFVÁNVÓSFÞPAPEDKKPLTRLÓÐRLIKKLGEHÁYPFTFBÍÞPNLÞC 125
                                  BEDEVMGINFORELCIASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTENISDNAPS
                                                                                                          Similarity
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                           Page 46; 47pp; English.
                                                                                                       45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "putative phosphorylation-recognition region"
                                                                                          Score 903.5; DB 4;
Pred. No. 4.2e-85;
6; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dent arrestin mutant;
GPCR ligand; retinitis pigmentosa;
                                                                                         Indels
                                                                                                        Length 418;
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음 衫 В

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The invention relates to a complex of protein-protein interactions (forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polynucleotides in adipocytes encoding for the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the creation of which is toxic for the recombinant host cell which is captression of which is toxic for the recombinant host cell which is creating the modulating observed and a reporter gene the polynucleotide encoding a first hybrid polypeptide and by brinding domain the second vector comprising a polynucleotide encoding a first hybrid polypeptide shinteract and selecting the modulating compound which inhibits the growth of the selecting the modulating compound which inhibits the growth of the complexes are useful for identification compounds that two-hybrid system). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; yeast two-hybrid assay; adipocyte; bait protein; NIDDM; non-insulin diabetes mellitus; obesity; selected interacting domain; SID; protein-protein interaction map; PIM; anorectic; metabolic disorder.
                                                                                                                                                                                                                                                                                                                            Claim 1; Page 52; 125pp; English
                                                                                                                                                                                                                                                                                                                                                            Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions useful for treating obesity and metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JAN-2001; 2001US-0259377P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Legrain
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Best Local S
Matches 179
 21-OCT-2002
                                                                        ABG70174 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    obesity or metabolic diseases. The interactions between the proteins of the complex further define a set of selected interacting domains, SID. The present sequence represents a member of the protein complex of the invention, used as the bait protein in the yeast two- hybrid assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The compound isolated by the method is useful for treating and preventing obesity or metabolic diseases. The interactions between the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein interactions and useful for treating obesity and metabolic
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                                                                                                                                                                    EVPEHETPVDTNLIELDTND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVFKKASPNGKLTVYLGKRDFVDHIDLVEPVDGVVLVDPEYLKE-RRVYVTLTCAFRYGR
                                                                                                                                                                                                     KVIHADSQADVETFRODTID
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                                                                                                                                                                                                                                                                                                                                                                                     TTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVRQYADICLFN
                                                                                                                                                                                                                                                                                                                                                                                                                       VRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQ 245
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(first entry)
                                                                        protein;
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47.1%;
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Human prey protein for Shigella ipaH9.8

#4

RESULT 1:
ABG70174
ID ABG7
XX ABG7
XX ABG7
XX Prey
DT 21-(
DT 21-(
DT Ship Huma
XX Prey
DW WD20
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DW WO20
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XX Hom Prey protein; ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1; Shigella; shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid ayst protein-protein interaction; SID; selected interacting domain; human. WPI; 2002-599706/64. N-PSDB; ABS51567. 12-JAN-2001; 2001US-0261130P 11-JAN-2002; 2002WO-EP000777. WO200257303-A2 sapiens ۳. HYBRIGENICS system;

Claim 7; Page 117-118; 162pp; English.

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The invention relates to a complex of protein-protein interactions cC between a Shigella flexheri polypeptide (e.g. ospB, ospB, ipaD, ipaC, CC specification. The complexes are formed using the yeast two-hybrid cinteractions between the Shigella flexneri polypeptide defined in the cC interactions between the Shigella flexneri polypeptide and a mammalian polypeptide and a mammalian compound that inhibits or activates the protein-protein interactions, (2) selecting a modulating compound obtained from the method of (2); (4) a SID cc a modulating compound obtained from the method of (2); (4) a SID cc compound the human polypeptides appearing as ABG70042-ABG70242; (5) a containing the vector; and (10) a protein comprising the vector; and (10) a protein comprising the containing the vector; and (10) a protein comprising should be specification. A pharmaceutical composition comprising Shigella cc specification: A pharmaceutical composition comprising Shigella cc shigellosis (bacillary dysentery) in a human or mammal. The present cassay, forming a complex of the invention with a shigella protein hybrid
                                                            Antagonist of cell cycle progression polypeptide #108.
                                                                                                                                                                                                                                                                                                                                                                 246 TAQYKCFVAMEBADD--TVAÞSSTFCKVYTLÍÞFLANNREKRGLÁLÐGKLKHEÐTNLASS
                                                                                                                                                                                                                                                                                                                                                                                246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 VRKDFMLSPGBLELEVTLDKOLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New complex of protein-protein interactions between a bait Shigella flexneri polypeptide and a prey mammalian or human placenta polypeptide for treating or preventing bacillary dysentery in a mammal or human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 ŚVTLÓPÓPEDTĠKAĊĠVDYEVKAFCAENLEEKIHKŃNSVRĹVÍRKVQYÁÞERPGPŐÞŤAB 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQEAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                 TLLREGANREILGIÍVSÝKVKVKLVVSRGGLLGDLASSDVAVELÞFTLMHÞKÞKEEPPHR
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                                                                                                                                                                                                                                                                                                                                                                                                                            TTRQFLMSDKPĹHĹĖASĹĎKEIŸYĤĠĖPÍSVŇVHVTŇŇTŇKTVKKÍKISVRÓYAĎICĹÉN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDLDVLGÍTFRKOLFVÁNVÓSFÞPAPEDKKPLTRLÓERLIKKLGEHÁYÞFTÞEÍÞÞNLÞC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.6%; Score 900.5; DB 5; Length , 46.8%; Pred. No. 8.6e-85; tive 77; Mismatches 112; Indels
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 418 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Sim:
                    364
                             356 KVIHADSQADVETFRQDTID 375
                                    304 TLLREGANKEILĠIİVSYKYKYKLVVSRGGLLĠDLASSDVAVELPETLMHPKPKBEPPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 216; 461pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cell cycle progression genes and proteins for modulating cell cycle progression in cells, for preventing, treating or diagnosing cell cycle proliferative diseases (e.g. cancer) or for identifying modulators of
                                                                                                                             246 NGSYRNTVASLETSEGCPIOPGSSLOKVMYLTPLLSSNKORRGIALDGOIKRODOCLAST 305
                                                                                                   246 TAQYKCPVAMEEADD--TVAÞSSTFCKVYTLTÞFLANNREKRÓLÁLDGKLKHEDTNLÁSS
                                                                                                                                                                186 TTROFLMSDKPĹHĹĖASĹĎKEIŸYĤĠĖPĹSVŇVHVTŇŇTŇKTÝKKÍKISVRÓYAĎICĹFN 245
                                                                                                                                                                                        186 VRKDEMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLEQ 245
                                                                                                                                                                                                                                                          126 SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
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06-MAY-2003; 2003US-0488402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-DEC-2003; 2003WO-GB005635
                                                                                                                                                                                                                                                                                                 66 ÉDLDVLGÍTFRKDÍFVÁNVÓSFÞÞAPEDKKPLTRÍÐÉRÍIKKLGEHÁYÞFTÞEÍÞÞNLÞC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004063362-A2
EVPENETPVDTNLIELDTND 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; cancer; cell division cycle; mitosis; meiosis; cell cycle progression.
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                                                                TLLAQPDQRDAFGVIISYAVKVKLFL--GALGGELSA-----BLFFVLMHPKPGTK---A 355
                                                                                                                                                                                                                                                                                                                                                                 7 RVFKKASPNGKLTVÝLGKKDFVDHIDLVDÞVDGVVLVDÞEYLKE-RRVYVTLTCAFRYGR
                                                                                                                                                                                                                                                                                                                                                                                  6 KVFKKCAPNGKVTLYMGKRDFVDHVSGVEFIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR 65
                                                                                                                                                                                                                              ŚVTĹÓPÓPEDTGKACGVDYEVKAFCAENLEEKIHKRNSVRĽVÍŘKVOYAPERPÓPÓPTAE 185
                                                                                                                                                                                                                                                                                                                       EEDEVMGLNFOKELCLASEQIYPRPEKSDKEOTKLQERLLKKLGSNAIPFTENISPNAPS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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46.8%; Pred. No. 8.6e-85;
ative 77; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 13;
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S

66

Matches Query Match Best Local

Similarity

Conservative

RESULT 12
ADQ89786
ID ADQ89
XX ADQ89
XX ADQ89
XX ADQ89
XX ADQ89
XX ADQ89
XX ADQ89
XX ADQ89
AT 21-OCT
XX ATAGG

ADQ89786 standard; protein; 418

21-OCT-2004

(first entry)

В Ś B Ś Д Ś 밁 Ş 뭐 Ś 밁 Ş В

304

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RESULT 13
AAG67779
ID AAG67779
XX AAG67779
XX AAG67
XX AAG67
XX AATE
XX AFT
XX AFT
XX AFT
XX AFT
XX AFT
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                                                                                                                                                                          comprises contacting a composition comprising the GPCR and a constitutively active arrestin mutant with a test compound; and contential lity of the test compound to modulate binding of carrestin mutant to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is used for identifying potential ligands and/or modulators of GPCRs, particularly modulators, for use as human therapeutics. Modulators of GPCRs, particularly modulators, for use as human therapeutics. Modulators of GPCRs, beta tionary night blindness, colour blindness, nephrogenic DI, isolated glucocorticoid deficiency, hyperfunctioning thyroid adenomes, familial hypocalciuric hypercalcemia, hyperparathyroidism and neurological disorders. The methods may be used for screening pluralities of test compounds (e.g. a small molecule library of compounds) or a composition containing a colourality of GPCRs. The methods may be used in screening assays for identification of natural and surrogate agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    describes phosphorylation-independent arrestin mutants. These mutar used in screening assays to identify ligands and/or modulators of c protein-coupled receptors (GPCRs). A method for identifying a GPCR protein-coupled receptors (GPCRs).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a G protein-coupled receptor ligand, useful for treating retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigm
stationary night blindness; colour blindness; nephrogenic DI;
isolated glucocorticoid deficiency; hyperfunctioning thyroid
familial hypocalciuric hypercalcemia; hyperparathyroidism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-602637/68.
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                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening assays.
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155. .184
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45.5%; Score 897.5; DB 4;
46.8%; Pred. No. 1.8e-84;
tive 76; Mismatches 113;
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The invention relates to isolated polynucleotide (I) and polypeptide (I sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also use in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal
                                                                                                       The invention sequences. (I)
                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, u diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and t
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
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2000US-00649167.
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medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                      NO 43933; 103pp;
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                                                                                                                                                                                                                                                                                                    mutations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity of (II) or to treat disease states involving (II). (II) is Cuseful for generating antibodies against it, detecting or quantitating a foot pypeptide in tissue, as molecular weight markers and as a food consists expressing (II). (I) and (II) are useful in medical imaging CC involving aberrant protein expression or biological activity. The CC diagnostics, forensics, gene mapping, identifications in CC and to produce other types of data and polymore of the relation of mutations are calculated activity of the produce other types of data and products dependent on DNA and CC amino acid sequences of the invention. Note: The sequence data for this cC canno acid sequences of the invention. Note: The sequence data for this cC patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at CC electronic format directly from WIPO at
03-MAR-2000; 2000US-0186706P
                                 05-MAR-2001; 2001WO-US007304.
                                                                         13-SEP-2001.
                                                                                                                                                             Arrestin; phosphorylation-independent arrestin mutant; G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa; stationary night blindness; colour blindness; nephrogenic DI; isolated glucocortricoid deficiency; hyperfunctioning thyroid adenoma; familial hypocalciuric hypercalcemia; hyperparathyroidism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                          WO200167106-A2
                                                                                                                                           Unidentified.
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                                                                                                                                                                                                                                                                      An exemplary phosphorylation-independent arrestin mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAQYKCPVAMEEADD---TVAPSSTPCKVYTLTPPLANNREKRGLALLDGKLKHEDTNLASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC arrestin mutant. Such mutants are used in screening assays to identify comethod for identifying a GPCR ligand comprises contracting a composition comprising the GPCR and a constitutively active arrestin mutant with a CC comprising the GPCR and a constitutively active arrestin mutant with a CC modulate binding of arrestin mutant to the GPCR, where modulation of CC used for identifying better that the test compound is a GPCR ligand composition of CC used for identifying potential ligands and/or modulators of GPCRs, where modulation of CC GPCR may be used for treating potential ligands and/or modulators of GPCRs, where modulators of GPCRs attionary night bilindness, colour bilindness, nephrogenic DI, isolated CC disorders. The methods may be used for screening pluralities of test compounds (e.g. a small molecule library of compounds) or a composition contential splurality of GPCRs. The methods may be used for screening pluralities of test compounds (e.g. a small molecule library of compounds) or a composition cassays for identification of natural and surrogate agonists of orphan
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying a G protein-coupled receptor ligand, useful for treating retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for
                                                    247 TAQÝKCPVÁQLÉQDD--QVSPSSTFCKVYTIŤÞLLSDNREKRGLÁLDGKLKHEDTNLÁSS
                                                                         246 NGSYRNTVASLETSEGCPIQPGSSLQKVWYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305
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TIVKEGANKEVLGILVSYRVKVKLVV-SRGGDVSVELPFVLMHPKP
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                         TLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELFFVLMHPKF 351
                                                                                                                                   TTRHFLMSDRSĹHĹĖASĹĎŔEĹŶYHĠĔPLNŶŇVHVTŇŇŚTŔTŶŔŔĬŔVSVRQYAĎICĹĖS
                                                                                                                                                                           ŚVTLÓPĠPEĎTĠKAĊĠVDFEIRAFCAKŚLEEKSHKŔNSVRĹVIŔKVQFÁPEKPGPQPSAE
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                                                                                                                                                                                                                                       BDLDVLGLSFRKDLF1ATYQAFÞÞVÞNÞÞRÞÞTRLQDRLLRKLGQHÁHÞFFFTTIPQNLÞC
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48.3%; Pred. No. 3.1e-83;
7ative 77; Mismatches 98;
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Maximum Match 100%
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                seq length: 0 seq length: 2000000000
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Query
Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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1973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyright
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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  SUMMARIES
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664.897 Million cell updates/sec
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Sequence 58832, A
Sequence 43475, A
Sequence 43475, A
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Matches 176; Conserv
                                                                          246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST
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                                                              TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASS
                                                                                                     TTROFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVROYADICLFN
                                                                                                                                                      SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
    QADVETFRQDTID 375
                                                                                                                                             SVTLOPGPEDTGKACGVDYEVKAFCAENLEEKIHKRNSVRLVIRKVOYAPERPGPOPTAE
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
84	84	84.5	84.5	84.5	84.5	85	85	85	85	85.5	85.5	86	86	86	86.5	86.5	86.5
4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.4	4.4	4.4	4.4		4.4
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US-08-296-791-5	US-09-248-796A-14855	US-09-902-540-10641	US-09-489-039A-14257	US-09-543-681A-7520	US-09-134-001C-4817	US-09-252-991A-24829	US-09-012-871-2	US-08-843-521-2	US-09-270-767-43701	US-09-107-433-4536	US-09-583-110-2916	US-09-538-092-867	US-09-422-869-22	US-09-248-796A-19232	US-09-091-117-2	US-09-651-236-775	US-09-759-143-775
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
5, Appli	14855, A	10641, A	14257, A	7520, Ap	-	24829, A	2, Appli	2, Appli	43701, A	4536, Ap	2916, Ap	867, App	22, Appl	19232, A	2, Appli	775, App	775, App

ALIGNMENTS

Sequence 3, Application US/09880137 Sequence 3, Application US/09880137 Patent No. 6640025 GENERAL INFORMATION: APPLICANT: Berstein, Gabriel TITLE OF INVENTION: METHODS OF ASSAYING FOR G TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIC FILE REFERENCE: MNI-131 CURRENT APPLICATION NUMBER: US/09/880,137 CURRENT FILING DATE: 2001-03-05 PRIOR APPLICATION NUMBER: US 60/186,706 PRIOR FILING DATE: 2000-03-03 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 410 TYPE: PRT ORGANISM: Homo sapiens 46.0%; Score 907.5; DB 4; llarity 47.2%; Pred. No. 2.7e-87; Conservative 78; Mismatches 112; LIGANDS AND MODULATORS Length 410; 7;

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Sequence 2, Application US/09880137
Patent No. 6640025
GENUREAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR PILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
OFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1. Application US/09880137
Patent No. 6640025
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
ITILE OF INVENTION: METHODS OF ASSAYING FOR G
ITILE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US/09/880,137
PRIOR APPLICATION NUMBER: US 60/186,706
NUMBER OF SEQ ID NOS: 8
SOFTMARE: FastSEQ for Windows Version 4.0
LENGTH: 418
TYPE: PRT
GRANISM: Bos taurus
US-09-880-137-1
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US-09-880-137-2
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Matches 179;
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                                                                                                                                                                                                                                                                                                         356 KYIHADSQADVETFRQDTID 375
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                                                                                                                                                                                                                                                                                                                                                                                     246 TAQÝKCPVÁMEÉADD---TVAPSSTFCKÝYTĹŤPFĹANNREKŘÍCLÁĽDÍKLKHEDTNÍÁSS
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Similarity 47.1%; Score 903.5; DB 4; Length 418;
79; Conservative 76; Mismatches 112; Indels 13;
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CURRENT APPLICATION NUMBER: US/09/880,137

CURRENT FILING DATE: 2001-03-05

PRIOR APPLICATION NUMBER: US 60/186,706

PRIOR APPLICATION NUMBER: US 60/186,706

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8
                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation US-09-880-137-8
                                                                                                                             Query Match

44.9%; Score 885; DB 4

Best Local Similarity 48.3%; Pred. No. 6e-85;

Matches 167; Conservative 77; Mismatches
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Patent No. 6640025
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTO
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LENGTH: 418
TYPE: PRT
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Best Local Similarity
67 ÉDLDVÍLÓLSÉRKOLFTÁTYQAFÉPVENPERPETRLÓDŘÍLKKLÍGOHÁHÉFFFTÍPQNLÉC 126
                                                                              6 KVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEXIRDNRKVFGQIVCSFRYGR
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                    EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVFKKSSPNCKLTVYLGKRDFVDHLDKVDFVDGVVLVDPDYLKD-RKVFVTLTCAFRYGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVFKKASPNGKLTVYLGKRDFVDHIDLVDFVDGVVLVDPEYLKE-RRVYVTUTCAFRYGR
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46.8%; Pred. No. 3.3e-86;
ative 76; Mismatches 113;
                                                                                                                                                       DB 4; Length 382
                                                                                                                                  98;
                                                                                                                                                                                                                                                                                                                                                                                                     LIGANDS AND MODULATORS
                                                                                                                            Indels
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APPLICANT: BETSTEEIN, GABTIEI
APPLICANT: BETSTEEIN, GABTIEI
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIC
FILLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIC
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 4
RESULT 6
US-09-880-137-7
; Sequence 7, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
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US-09-880-137-4
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; TYPE: PRT
; ORGANISM: Homo sapiens
U8-09-880-137-4
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                                                                                                                                                                                                                                                                                                                                      127
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al Similarity 48.3%;
167; Conservation
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                                                                                                                                                                                                                              NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77; Mismatches
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Pred. No. 6.6e-85;
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APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

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US-09-949-016-8383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8383, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.0%; Pred. No. 2.2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
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TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: MNI-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAQYKCPVAQLEQDD--QVSPSSTFCKVYTITPLLSDNREKRGLALDGKLKHEDTNLASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIVKEGANKEVLGILVSYRVKVKLVV-SRGGDVSVELPFVLMHPKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVFKKSSPNCKLTVYLGKRDFVDHLDKVDFVDGVVLVDFDYLKD-RKVFVTLTCAFRYGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVTLQPGPEDTGKACGVDFEIRAFCAKSLEEKSHKRNSVRLVIEKVQFAPEKPGPQPSAE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDLDVLGLSFRKDLFTATYQAFPPVPNPPRPPTRLQDRLLRKLGQHAHPFFFTTPQNLPC
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Pred. No. 2.2e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGANDS
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Query Match

43.3%;

Score 853.5;

멂

4;

Length 401;

297

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PATERIAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMCRPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/349,016
PRIOR APPLICATION NUMBER: US/09/349,016
PRIOR PRILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 2000-09-08
INUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-949-016-8384
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8384,
                                                                                                                                                                                                                          / Match
Local Similarity 46.1%; Score 853.5; DB 4; Length 401;
Local Similarity 46.1%; Pred. No. 1.4e-81;
hes 170; Conservative 75; Mismatches 111; Indels 13;
                                              137 GDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTLVRKDFMLSPGE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 46.1
hes 170; Conservative
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                        GKAĆĠŶDYEVŔAĖCAĖNLEEKTĖKRNSŸRĹVİRKVQYAPERPGPQPTAETTRQFLMSDKP 179
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                                                                                        KBLCLASEQIYPRPEKSDKEQTKLQERLIKKLGSNAIPFTFNISPNAPSSVTLQQGEDDN 136
                                                                                                                                                        LÍVÝLGKŘÓ ÞVDHIDL VD ÞVDGVVL V DPBÝLKE - ŘR VYVTLT ČA FRÝGŘÉDLDVLGLTFR
                                                                                                                                                                            VTLYMGKRDFVDHVSGVEFIDGIVVLDDEYIRDNRKVFGQIVCGFRYGREEDEVMGLNFQ 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384, Application US/09949016 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EADD--TVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASSTLLREGANREI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHLEASLDKEIYYHGEDISVNVHVTNNTNKTVKKIKISVRQYADICLENTAQYKCDVAME 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQNGSYRNTVASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTLVRKDFMLGBGE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPSSVTLQQGEDDN 136
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75; Mismatches 111; Indels
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 388
TYPE: PAT
ORGANISM: Homo sapiens
US-09-880-137-6
RESULT 10
US-09-880-137-5
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US-09-880-137-6
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Best Local
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Patent No. 6640025
GENERAL INFORMATION:
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TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
                                                                   359
                                                                                                                                                                 305
                                                                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                                               122 CŚVTĹÓPĠPĖĎAGKPĊGIDFEVKSFCAENPESTVSKŔDYVRĹVVŔKVÓFAPPEAGPGPSA 181
                                                                                                                                                                                                                                                                                                                                    125 SSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQPAPTKQGQQPCT 184
                                                                                                                                                                                                                                                                                                                                                                                 62 DDLEVIĞİTFRKDİYVQTLQVVPAESSSPQGALTVLQERLLHKLĞDNAYEFTLQMVTNLF
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298 LGIIVSYKVKUKLVVSRGGLLGDLASSDVAVELPFTLMHPKPKEEPPHREVPENETPVDT 357
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                                                                            IHADSQADV---ETFRQDTIDQQASVDFE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257
                                                                                                               STIIRPGMDKELLGILVŠÝKVKVNÍMVSCGGILGDÍTÁSDVGVŘÍPLVÍJHPŘPSHEÁA-
                                                                                                                                            TTLLAQPDQRDAFGVIISYAVKVKLFL--GALGGELSA-----ELPFVLMHPKPGTKAKV 357
                                                                                                                                                                                                   QNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAS 304
                                                                                                                                                                                                                                                                 SLDKÝTKTÝFIQEFTE--TVAANSSFSQSFAVTPILAASCQKRGLÁLDGKLKHEDTNLÁS
                                                                                                                                                                                                                                             QTIRRĖLĖSAQDĖQĖQAMMDREVHYHGEPISVNVSINNCTNKVIKKIKISVDQITDVVLY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      EEDEVMGINFQKELCLASEQIYPRPEKSDK-EQTKLQERLLKKLGSNAIPFTFNISPNAP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVFKKCAPNGKVTLYMGKRDFVDHVSGVEDIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                               ÉADD---TVAÞSSTFCKVYTLTÞFLANNREKRGLÁLDGKLKHEDTNLÁSSTLLREGANREI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.6%; Score 780.5; DB 4; Length 388; 42.7%; Pred. No. 7.3e-74; Live 79; Mismatches 125; Indels 19;
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SEQ ID NO 5

LENGTH: 388

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-137-5
                                                                      PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REPERENCE: CLOO1307
CURRENT APPLICATION UNMEER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
                SOPTWARE: FastSEQ for Windows Version SEQ ID NO 9940 LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                        Sequence 9940, Ap
Patent No. 681233
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 IHADSQADV---ETFRODTIDQQASVDFE 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 39.5%; Score 779.5; DB 4; Similarity 42.4%; Pred. No. 9.3e-74; 65; Conservative 80; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLDKYTKTVFIQEFTE--TVAANSSFSQSFAVTFILAASCQKRGLALDGKLKHEDTNLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLF 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTIRRFLLSAQPLQLQAWMDREVHYHGEPISVNVSVNNCTNKVIKKIKISVDQITDVVLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDLEVIGLTFRKDLYVQTLQVVPAESSSPQSPLTVLQERLLHKLGDNAYPFTLQMVTNLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SSEDIVIEEFTRKGEEESQKAVEAE 383
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OF DETECTION
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US-09-270-767-43475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-270-767-58832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                       Sequence 43475, Appl. Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58832, Appearent No. 6703491
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                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
FILE REFERENCE: FILE REFERENCE: VS/09/270,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                  235 VQQGVDVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQ 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
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                                                                                                                                                                                                                                                                         295 IKRQDQCLASTTLLAQPDQRDAFGVIISYAVKVKLFLGA--LGGELSAELPFVLMHPKP
                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
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                                                                                                                                                                                                                                  LKHEDTNLASSTLITNPAQRESLGIMVHYKVKVKLLISSPLLNGDLVAELPFTLMHPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305
                                                                                                                                                                                                                                                                                                               X.
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                                                                                                                                    Application
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                                                                                                                                                                                                                                                                                                                                                                                                Score 316; DB 4; 1
Pred. No. 4.3e-25;
5; Mismatches 33;
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Pred. No. 1.2e-72;
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melanogaster

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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
LENGTH: 137
                                                                                                                          RESULT 15
US-09-270-767-47598
, Sequence 47598, Application US/09270767
, Patent No. 6703491
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Drosophila melanogaster
US-09-270-767-32381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32381, Application US/09270767
Patent No. 6703491
Patent No. 6703491
PATENTION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster CURRENT APPLICATION NUMBER: US/09/270,767
PULMEROT FILING DATE: 199-03-17
SOFTMARE: Patentin Ver. 2.0
LENGTH: 137
TYPE: PRT
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US-09-270-767-43475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43475
LENGTH: 475
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ORGANISM: Drosophila melanogaster
FEATURE:
                                                                                                                                                                                                                                            136 AP 137
                                                                                                                                                                                                                                                                     123 AP 124
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                                                                                                                                                                                                                                                                                          64 GREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQ-TKLQERLLKKLGSNAIPFTENISPN 122
                                                                                                                                                                                                                                                                                                                              :|:|| :|| :||: |:
19 RVYKKTSENCVLTLXLPTREIT--LTGNNPSVLRGIVYVDPKAIQGYR-VYAQLTLTFRY 75
                                                                                                                                                                                                                                                                                                                                               6 KVFKKCAPNGKVTLYMGKRDFVDHVSGVEP--IDGIVVLDDEYIRDNRKVFGQIVCSFRY 63
                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 VQQQVDVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQ 294
                                                                                                                                                                                                                                                                         ĠŔĖDEĖVNĠĹŖĖCNĖAIMSLHQIWĖRLĖEPTPĖSLSPLOĖALMKRLĠDGAHĖFTLSLŚSY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59;
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        11.4%; Scc
42.6%; Pre
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49.6%; Pro
ative 25;
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Pred. No. 1.1e-15;
6; Mismatches 38
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Pred. No. 1.7e-24;
25; Mismatches 33
                                                                                    of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                              38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 137;
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; ORGANISM: Drosophila melanogaster
US-09-270-767-47598
                                                                                                                                                Matches
                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                          Local
136 AP 137
                    123 AP 124
                      76 GREDEEVMGLRFCNEAIMSLHQÍWÞRLEEPTPESLSÞÍQEALMKRÍGDGÁHÞFTLSLSSY 135
                                   64 GREEDEVMGINFQKELCLASEQIYPRPEKSDKEQ-TKLQERLLKKLGSNAIPPTFNISPN 122
                                                                       19 RVYKKTSPNCVLTLYLPTREIT--LTGNNPSVLRGIVYVDPKAIQGYR-VYAQLTLTFRY
                                                                                        6 KVFKKCAPNGKVTLYMGKRDFVDHVSGVEP--IDGIVVLDDEYIRDNRKVFGQIVCSFRY 63
                                                                                                                                                     Similarity
                                                                                                                             11.4%; Score 225; DB 4; I
42.6%; Pred. No. 1.1e-15;
Conservative 26; Mismatches 38;
                                                                                                                                                 Length 137;
                                                                                                                              Indels
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                                                                                                                         Gaps
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Search completed: February Job time : 45 secs

9, 2005,

23:55:39

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 0.5
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1973
                                                                                                                                                                                                                                                                                                                                                                                    1373511 seqs, 325702437 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQQASVDFE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyright
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

13	12	11	10	9	89	7	6	ຫ	4	u	2	-	Result
885	897.5	897.5	900.5	903.5	903.5	903.5	907.5	907.5	982.5	1023	1973	1973	Score
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382	418	418	418	452	418	418	410	410	401	398	383	383	Query Match Length DB
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US-09-880-137-8	US-09-800-137A-2	US-09-880-137-2	US-10-043-487-348	US-10-038-010-52	US-09-800-137A-1	US-09-880-137-1	US-09-800-137A-3	US-09-880-137-3	US-10-094-240-27	US-10-094-240-25	US-10-056-405-2	US-10-094-240-2	ID
Sequence 8, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 348, App	Sequence 52, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 27, Appl	Sequence 25, Appl	Sequence 2, Appli	Sequence 2, Appli	Description

Sequence 15,	_	356		90	45
Sequence 201424,	_	976			44
Sequence 58846,	US-10-282-1221	492		90.5	43
~	US-09-881-752A-142	492	4.6	0	42
Sequence 3534	US-10-104-047-353	800		91	41
ø	US-10-369-493-2030	498		91	40
Sequence 1062	US-09-815-242-10623	698	4.6		39
Sequence 11525	US-10-43	752		91.5	38
	US-10-28	416		:	37
	US-1	299	4.6	۲.	36
	US-10-282-122A-5687	1348			35
	US-1	944		92	34
	US-10-335	320		92	33
	US-1	1211	٠	94.5	32
	US-1	348		95	31
	US-10	1632		98.5	30
e 58	US-10-335-977-5814	349		98.5	29
407	9 US-09-864-761-40768	38	5.6	111	28
453	US-09-864-761-45375	65		7	27
Sequence 4673, Ap		212	•	361.5	26
μ	16 US-10-722-357-31	466			25
5	US-09-800-137A-5	388		•	24
Sequence 5, 1	US-09-880-137-5	388		٠	23
е 6	US-09-800-137A-6	388	39.6	780.5	22
Sequence 6, Appli	US-09-880-137-6	388			21
ŋ	US-10-369	454		865	20
	-su	410		869.5	19
œ	US-09-800-137A-7	409		B	18
7, 1	US-09-880-137-7	409		æ	17
Sequence 4, Appl	US-09-800-137A-4	409		885	16
Sequence 4, A	US-09-880-137-4	409	44.9	æ	15
Conference of which	TO 00-03-000-10/A-0	000	44.7	000	14

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 383
TYPE: PRT
ORGANISM: Anopheles gambiae
US-10-094-240-2
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Publication No. US20030082637A1
GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
FILE REFERENCE: N8289
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 383; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/094,240 CURRENT FILING DATE: 2001-03-08 PRIOR APPLICATION NUMBER: 10/056,405 PRIOR FILING DATE: 2002-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/264,649 PRIOR FILING DATE: 2001-01-26
121 PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                   61
                                                                                         61 FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120
                                                                                                                                                   1 MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
                                                                                                                                                                            1 MYNPKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
                                                                PRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS
                                                                                                                                                                                                                                 100.0%; Score 1973; DB 14; ilarity 100.0%; Pred. No. 4.4e-176; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                              Length 383;
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10-056-405-2

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Sequence 2, Application US/10056405

Publication No. US20030166013A1

APPLICANT: ZWIEBEL, LAURENCE J.

TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS OF FILE REFERENCE: N7841

CURRENT APPLICATION USE THEREOF

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR APPLICATION NUMBER: 60/264,649

SOFTMARE: PATEN DATE: 2001-01-26

SOFTMARE: PATENT DATE: 201-01-26

LENGTH: 383

TYPE: PRT

ORGANISM: Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Score 1973; DB 14; Length 383;
Matches 383; Conservative 0; Mismatches 0; Indels 0;
                                                                                        361 bsoabverrkobribooasvbre 383
                                                                                                                 301 ČĹAŚTTĹĹĀÓĖĎÓRĎĀĖĠVĬĬŚYĀVKVKĹĖĽĠĀĹĠĠĒĹŚĀĒĹÞĖVLMHPKPĠTKĀKVÍHĀ 360
                                                                                                            361 DSQADVETFRODTIDQOASVDFE 383
                                                                                                                                  301 CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA 360
                                                                                                                                                                     241 VVLFQNGSYKNTVASLETSEGCÞÍQÞGSSLÓKVMYLTÞLLSSNKÓKRGÍÁLÞGQÍKRÓÞÓ 300
                                                                                                                                                                                          241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTDLLSSNKQRRGIALDGQIKRQDQ 300
                                                                                                                                                                                                                           181 QPCTLVRKDFWLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKWYKKIKAMVQQGVD 240
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RESULT 4

US-10-094-240-27

Sequence 27, Application US/10094240

Fublication US/0030082637A1

FUBLICANT: ZWIEBEL, LAURENCE J.

FILE REFERENCE: MASA

CURRENT APPLICATION NUMBER: US/10/094,240

FRIOR APPLICATION NUMBER: US/10/094,240

FRIOR APPLICATION NUMBER: US/10/094,240

FRIOR FILING DATE: 2001-03-08

FRIOR APPLICATION NUMBER: US/10/094,240

FRIOR PILING DATE: 2002-01-24

FRIOR APPLICATION NUMBER: 00/264,649

SOFTWARE: SEQ ID NOS: 27

LENGTH 401
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US-10-094-240-25
Sequence 25, Application US/10094240
Publication NG20030082637A1
GENERAL INFORMATION
APPLICANT: ZWIEBEL, LAURENCE J.
FILE REFERENCE: NB289
TITLE OF INVENTION: ARESTIN GENE, PO:
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FURIES FILING DATE: 2001-03-08
FRIOR APPLICATION NUMBER: 10/056,405
FRIOR FILING DATE: 2002-01-24
FRIOR APPLICATION NUMBER: 60/264,649
FRIOR APPLICATION NUMBER: 60/264,649
FRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 27
SECTIMARE: Patentin Ver. 2.1
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I TYPE: PRT
ORGANISM: Anopheles gambiae
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Best Local Similarity
Matches 204; Conserv;
                                                                                                                                                                                                                                                             358 VNALKKMKSIĖRHRYENSHYADDDDNIVĖĖ 387
                                                                                                                                                                                                                                                                                       357 VIHADSQADVETERQDT----IPQQASVDFE 383
                                                                                                                                                                                                                                                                                             298 VNÍASSTÉISEGKCPSDAMGIVÍSÝSLRVKINCGTÉGGELQTDVÞFKIMNÞAÞGSVERER 357
                                                                                                                                                                                                                                                                                                                      300 QCLASTTLLAQED-QRDAFGVIISYAVKVKLFLGALGGELSAELFFVLMHFKPGT--KAK 356
                                                                                                                                                                                                                                                                                                                                                   239 EVTMV-NAQESKHIASLETREGCPITPGASFTKSFELVPLASSNKDRRGIALDGHLKEDD 297
                                                                                                                                                                                                                                                                                                                                                                     240 DVVLFQNGSYRNTVASLETSEGCPIOPGSSLOKVMYLTPLLSSNKORRGIALDGOIKROD 299
                                                                                                                                                                                                                                                                                                                                                                                                        179 RLPSSLVSKGFTFSQGKINLEVTLDREITYHGEKIAANIVVTNNSRKTVKSIKCFVVOHC 238
                                                                                                                                                                                                                                                                                                                                                                                                                           181 Q-PCTLVRKDEMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNIOMVKKIKAMVOQGV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 SNÁPSSVTLOAGEDDTGKÉLGVEVAIKAHVGEDESDKGHKRSAVTLTIKKLOYAPVSRGR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 PNAPSSVTLOOGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIOFAPTKOGO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 YRYGREEDEVNGVKFSKEMVLTKEQIYPM-ENANMEMTPMQERLVKKLGANAFPFTFHFP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FRYGREEDEVMGLNFOKELCLASEQIYBRPEKSDKEQTKLOERLLKKLGSNAIPFTFNIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MVVAVKVÉKKSAENGKLÍVÝLGKKDETDHTDYCDEÍDGVÍVLDEBÝLR-GRKVÉGOLÍTT 59
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ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.8%; Score 1023; DB 14; Length 398;
52.3%; Pred. No. 5.3e-87;
tive 65; Mismatches 111; Indels 10
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GENERAL INFORMATION:

APPLICANT: Bestevin, Gabriel

TITLE OF INVENTION: METHODS OF ASSAYING FOR G

TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIC

PILLE REFERENCE: MNI-131

CURRENT APPLICATION NUMBER: US/09/880,137

CURRENT FILING DATE: 2001-03-05

PRIOR APPLICATION NUMBER: US 60/186,706

PRIOR FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 8

SOPTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 410

TYPE: PRT
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US-09-880-137-3
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; ORGANISM: Drosophila melanogaster
US-10-094-240-27
                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09880137 Patent No. US20020031295A1
                                                                                                                                                                                                                                   Query Match
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Best Local
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-09-880-137-3
                                                                                                                                                                                                   Local Sir
126
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Similarity 48.7%; Pred. No. 3.3e-83;
91; Conservative 73; Mismatches 115; Indels 13;
                SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL
                                                            EDLDVLGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLJKKLGEHAYPFTFEIPFNLPC
                                                                                                                              KVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEXIRDNRKVFGQIVCSFRYGR
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RVFKKASPNGKLTVYLGKRDFVDHIDLVDPVDGVVLVDPEYLKE-RRVYVTLTCAFRYGR
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                                                                                BEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS 125
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                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                  46.0%; Score 907.5; DB 9;
47.2%; Pred. No. 3.7e-76;
vative 78; Mismatches 112;
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                                                                                                                                                                                                                                  Length 410;
                                                                                                                                                                                                     Indels
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; TYPE: PRT
; ORGANISM: Homo s
US-09-800-137A-3
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09800137A

Publication No. US20030157553A1

GENERAL INFORMATION:

APPLICANT: Berstein, Gabriel

TITLE OF INVENTION: METHODS OF ASSAYING FOR G

TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS

FILE REFERENCE: MNI-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Local Similarity 47.2%;
                                                363
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                                                                                                                                       TLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTK---AKVIHADS
                                                                                                                                                                                  TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASS
                                                                                                                                                                                                       NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305
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                                                PVDTNLIELDTND 375
                                                                              QADVETFRQDTID 375
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                                                                                                                 TILREGANREILGIIVSYKVKVKL-VESRGGDVAVELPFTLMHPKPKEEPPHREVPENET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 907.5; DB 10; Length 410; Pred. No. 3.7e-76;
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Indels

7;

Gaps

65

303

AND MODULATORS

US-09-880-137-1

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LENGTH: 418
TYPE: PRT
OGGANISM: Bos taurus
US-09-800-137A-1
                                               PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                            Sequence 1, Application US/09800137A

Publication No. US20030157553A1

APPLICANT INFORMATION:

TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILLE REFERENCE: NMI-131

CURRENT APPLICATION NUMBER: US/09/800,137A

DETTO ADDITION NUMBER: 2001-03-05

DETTO ADDITION NUMBER: 2001-03-05
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US-09-800-137A-1
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Fatent No. US20020031295A1

GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
ITITLE OF INVENTION: METHODS OF ASSAVING FOR G
FILE REFERENCE: MNI-131

CURRENT APPLICATION NUMBER: US/09/880,137

PRIOR APPLICATION NUMBER: US/09/880,137

PRIOR APPLICATION NUMBER: US/09/880,137

PRIOR FILING DATE: 2001-03-05

PRIOR FILING DATE: 2000-03-05

INUMBER OF SEG ID NOS: 8

SOFTWARE. Faster For Mindows
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LENGTH: 418
TYPE: PRT
ORGANISM: Bos taurus
US-09-880-137-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305
                                                                                                                                                                                                                                                                                                                                                                                                                             186 TTROFLMSDKPĹHĹĖASĹĎKBÍYVHĠEPÍSVŇVHVTŇNŤNKTVKKÍKISVROYAĎÍCLÉN 245
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47.1%; Pred. No. 9e-76;
tive 76; Mismatches 112; Indels 13
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ORGANISM: Homo sapiens
FEATURE;
NAME/KEY: beta Arrestin 1
LOCATION: (1). (452)
US-10-038-010-52
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Sequence 52, Application US/10038010

Publication No. US20030040089A1

APPLICANT: HYBRIGERICS

ITILE OF INVENTION:
APPLICANT: PLEATE, Legrain

FILE REFERENCE: B4767A

CURRENT APPLICATION NUMBER: US/10/038,010

PRIOR APPLICATION NUMBER: US/10/038,010

PRIOR APPLICATION NUMBER: US/002-07-23

PRIOR APPLICATION NUMBER: US/0038,010

PRIOR APPLICATION NUMBER: US/0038,010

PRIOR APPLICATION NUMBER: US/0038,010

PRIOR PILING DATE: 2001-07-23

PRIOR PILING DATE: 2001-07-23

PRIOR PILING DATE: 2001-01-02

SOFTWARE: Patentin version 3.1

LENGTH: 452

TYPE: PRI.

CRANTON.
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 179; Conserva
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126 SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
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Best Local Simi
Matches 179;
                                       66 ÉDLDVLGITFRKOLFVÁNVÓSFÉPAPEDKKPLTRÍ ÓÉRLÍKKLGEHÁVÉFTÉBÍ PÉNLEC 125
                                                      364 EVPEHETPVÖTNLIELÖTNÖ 383
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                                                                                                                                                                      Conservative
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79; Conservative
                                                                                                                                               45.8%; Score 903.5; DB 14; Length 452;
47.1%; Pred. No. 1e-75;
7ative 76; Mismatches 112; Indels 13;
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; ORGANISM: Shigella Flexneri
US-10-043-487-348
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US-10-043-487-348
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APPLICANT: Pierre, LEGRAIN
APPLICANT: Pierre, LEGRAIN
TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptid
TITLE OF INVENTION: mammalian polypeptides
TILE REFERENCE: B4778A
CURRENT PELICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SOFTWARE: PatentIn version 3.1
SEQ ID NO 348
LENGTH: 418
TYPE: NET
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               EVPENETPVDTNLIELDTND
                                                   KVIHADSQADVETFRQDTID 375
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     Sequence 2, Application US/09800137A
Publication No. US20030157553A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAVING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR 1
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/800,137A
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FABEUSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 418
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CURRENT APPLICATION NUMBER: US/09/880,137

CURRENT FILING DATE: 2001-03-05

PRIOR APPLICATION NUMBER: US 60/186,706

PRIOR FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

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LENGTH: 418
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Patent No. US20020031295A1
GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
TYPE: PRT
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les 178; Conserv
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46.8%; Pre
ative 76;
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Pred. No. 3.3e-75;
6; Mismatches 113;
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; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
FRIOR APPLICATION NUMBER: US 60/186,706
FRIOR APPLICATION NUMBER: US 60/186,706
FRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 409
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-137-4
Search completed: February 9, 2005, 23:44:23 Job time : 132 secs
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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ALIGNMENTS

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24-JAN-2002;
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2002US-00056405.
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The present invention describes a purified Anopheles gambiae olfaction polypeptide comprising a 393, 394, 380, 411, 412, 391, 157 or 401 residue amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively modified amino acid sequence of them, or a sequence of (S1) with at least 10 consecutive residues. Also described: (1) an isolated polymuclectide comprising: (a) a nucleotide sequence encoding the purified Anopheles gambiae olfaction polypeptide; or (b) a nucleotide sequence that hybridises under stringent conditions to a hybridisation probe comprising a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence (see ABQ75102 to ABQ75105 and ABQ75110 to ABQ7513) (S2), or its complement; and (2) a method for identifying an agent that binds to

New mosquito olfaction polypeptides and polynucleotides, useful for mosquito management, i.e. controlling the pest and disease vectors, for identifying pest control agents.

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Claim 18; Fig 2; 96pp; English.

WPI; 2002-627421/67. N-PSDB; ABQ75102.

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08-MAR-2002; 2002US-00094240
                                                                                                                                        10-MAR-2003; 2003WO-US007174.
                                                                                                                                                                                                                                    Arrestin 1; mosquito; olfaction; insecticide; antimalarial.
                                                                                                                                                                                                                                                                         Mosquito olfaction molecule, arrestin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mosquito olfaction molecules comprising: (a) providing an isolated isolated olfaction molecule; (b) contacting at test agent with the of the test agent to the isolated mosquito olfaction molecule; and (c) detecting specific binding olfaction-binding compound. The mosquito olfaction molecule, where the method from the present, i.e. controlling this pest and disease vector. A pest control agents. The present invention of screening for substances that the pest control agents. The present sequence represents a mosquito modulate arrestin-odourant receptor interaction is substances that the pest control agents. The present sequence represents Anopheles gambiae
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                                   pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the protein sequence of arrestin 1, a novel CC mosquito olfaction molecule. The invention provides 9 novel mosquito CC polypeptides and the nucleic acids encoding them. These are arrestins 1 CC and 2 and odorant receptor molecules 1-7. The odorant receptors function of a signal transduction pathway for the activation of CC mosquito olfaction. Arrestin functions to inhibit the activated signal cransduction to accade. Thus, the odorant receptors act as an 'on' switch of CC mosquito. Methods are provided for identifying compounds that indevided for identifying compounds that interfere CC compounds that modulate arrestin 2 activity. These are useful for the cc control of mosquitoes, particularly by reducing their ability to locate xx xx
                                                                                                          26-MAR-2002
                                                                                                                                     ABB61736;
                                                                                                                                                  ABB61736 standard; protein; 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mosquito arrestin 1 and 2 genes and polypeptides, useful for identifying mosquito olfaction molecule binding compounds which reduce the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 2; 101pp; English.
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N-PSDB;
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                                                                                                                                                                                                                       DSQADVETFRODTIDOQASVDFE 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383;
                                                                                                                                                                                                                                                                                                                 VVI. PONOS YRNTVAŠTETS BĠĆPI OPGSSI OKVMYLTPLLSSNKORRGIALDGOIKRODO
                                                                                                                                                                                                                                                                                                                                 VVLFQNGSYRNTVASLETSEGCEIQEGSSLQKVMYLTELLSSNKQRRGIALDGQIKRQDQ 300
              developmental biology; cell signalling; insecticide;
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83; Conservative
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DB; ACF79716.
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Score 383; Pred. No. 0; Mismatches

ВG 7; <u>,</u>

Length 383;

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WO2003076590-A2.

Anopheles gambiae

15-JAN-2004 ABR84476;

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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher sukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIG167-ABIG20511), expressed DNA sequences (ABIG1684-ABIG175) and the encoded proteins (ABIG177-ABIG177). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly for the printed specification, but was obtained in electronic format directly
  WPI; 2004-544089/52.
                                                       Glover D,
                                                                                                                                                                10-JAN-2003; 2003US-0439123P.
06-MAY-2003; 2003US-0468402P.
                                                                                                                                                                                                                                                  31-DEC-2003; 2003WO-GB005635
                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; cancer; cell division cycle; mitosis; meiosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antagonist of cell cycle progression polypeptide #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ89588 standard; protein; 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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11-JUL-2000;
                                                                                                              (CYCL-) CYCLACEL LTD
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DB; ABL05839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cycle progression.
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                                                       Bell G,
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2000US-00614150
                                                       Frenz
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100.0%; Pred. No. 1.2
tive 0; Mismatches
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                                                       Midgley
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a polynucleotide for preventing, treating or diagnosing a disease in an individual. The composition or the polypeptide, polynucleotide or RNA precursor, or antibody is useful for diagnosing, preventing or treating diseases (e.g. cell proliferative diseases such as cancer) in an individual. These may also be used for identifying substances capable of binding to or modulating the function of the polypeptide, capable of affecting the function of the corresponding gene, or capable of affecting the cell division cycle or cell cycle progression, preferably mitosis and/or meiosis. The present sequence represents an antagonist of cell cycle progression protein
                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigm stationary night blindness; colour blindness; nephrogenic D; isolated glucocorticoid deficiency; hyperfunctioning thyroid familial hypocalciuric hypercalcemia; hyperparathyroidism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 364 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cell cycle progression genes and proteins for modulating progression in cells, for preventing, treating or diagnosing proliferative diseases (e.g. cancer) or for identifying modulating modulations.
                                                                      Identifying a G protein-coupled receptor ligand, useful for treating retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for
                                                                                                                                                                                                                                                                                                                                                                               neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An exemplary phosphorylation-independent arrestin mutant
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                           Disclosure;
                                                                                                                                                                                                                            03-MAR-2000; 2000US-0186706P
                                                                                                                                                                                                                                                         05-MAR-2001; 2001WO-US007304
                                                                                                                                                                                                                                                                                         13-SEP-2001.
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                                                                                                                                    WPI; 2001-602637/68.
                                                                                                                                                                                              (MILL-) MILLENNUM PHARM INC
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                                                       screening assays.
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                           Page
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                           47pp;
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Pred. No.
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1.2e-10;
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present

sequence represents an exemplary phosphorylation-independent

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RESULT 6
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The present sequence is the protein sequence of arrestin 2, a novel mosquito olfaction molecule. The invention provides 9 novel mosquito polypeptides and the nucleic acids encoding them. These are arrestins 1 and 2 and odorant receptor molecules 1-7. The odorant receptors function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC ligands and/or modulators of G protein-coupled receptors (GPCRs). A comprising the GPCR and a constitutively active arrestin mutant for computating the GPCR and a constitutively active arrestin g a composition composition test compound; and determining the ability of the test compound to binding of arrestin mutant to the GPCR, where modulation of CC modulate binding of arrestin mutant to the GPCR, where modulation of CC without the cest compound is a GPCR ligand. The method is CC used for identifying potential ligands and/or modulators of GPCRs, where modulators of CC GPCR may be used for treating patients having e.g. retinits pigmentosa, CC stationary night blindness, colour blindness, nephrogenic DI, isolated CC glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial CC compounds (e.g. a small molecule library of compounds) or a composition containing a plurality of GPCRs in the methods may be used for screening pluralities of test cassays for identification of GPCRs. The methods may be used for screening or a composition of GPCRs, and for identification of GPCRs antagonists and/or agonists of orphan
                                                                                                   New mosquito arrestin 1 and 2 genes and polypeptides, useful for identifying mosquito olfaction molecule binding compounds which reduce the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.
                                                                                                                                                                                                                                                                                 08-MAR-2002; 2002US-00094240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arrestin 2; mosquito; olfaction; insecticide; antimalarial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mosquito olfaction molecule, arrestin 2.
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                                                                                                                                                                                      2003-722331/68.
DB; ACF79731.
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                                                                                        Fig 12b; 101pp; English.
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11; Conserv
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100.0%; Pr
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Query Match
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ABB61964
                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides in higher eukaryotes for the development of discloses genomic DNA sequences (ABL/6176-ABL/30511), expressed DNA sequences (ABL/6176-ABL/30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                    Disclosure; SEQ ID NO 12684; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 genes from Drosophila and for elucidating cell signaling and ce
                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
N-PSDB; ABL06067.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 12684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in a ligand-induced signal transduction pathway for the activation of mosquito olfaction. Arrestin functions to inhibit the activated signal transduction cascade. Thus, the odorant receptors act as an 'on' switch, and arrestin as an 'off' switch for the odorant detection system of the mosquito. Methods are provided for identifying compounds that interfere compounds that modulate arrestin 2 activity. These are useful for the control of mosquitoes, particularly by reducing their ability to locate sources of bloodmeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 398 AA;
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Similarity 2.9%; Score 11;
Similarity 100.0%; Pred. No.
11; Conservative 0; Mismatc
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The present sequence represents an exemplary phosphorylation-independent CC arrestin mutant. Such mutants are used in screening assays to identify CC ligands and/or modulators of G protein-coupled receptors (GPCRs). A CC method for identifying a GPCR ligand comprises contexting a composition CC comprising the GPCR and a constitutively active arrestin mutant with a CC comprising the GPCR and a constitutively active arrestin mutant with a CC compound; and determining the ability of the test compound to CC modulate binding of arrestin mutant to the GPCR, where modulation of CC binding indicates that the test compound is a GPCR ligand. The method is CC used for identifying potential ligands and/or modulators of GPCRs, CC particularly modulators, for use as human therapeutics. Modulators of GPCR may be used for treating patients having e.g. retinitis pigmentosa, CC stationary night blindness, colour blindness, nephrogenic DI, isolated CC glucocorticoid deficiency, hyperfunctioning thyroid acenomas, familial CC hypocalciuric hypercalcemia, hyperparathyroidism and neurological compounds (e.g. a small molecule library of compounds) or a composition of GPCRs, and for identification of natural and surrogate agonists of orphan CC GPCRs, and for identification of GPCR antagonists and/or agonists
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arrestin; phosphorylation-independent arrestin mutant; grotein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa; stationary night blindness; colour blindness; nephrogenic DI; solated glucocorticoid deficiency; hyperfunctioning thyroid adenoma; familial hypocalciuric hypercalcemia; hyperparathyroidism;
                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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RESULT 9
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                                                                                                  The present sequence represents an arrestin protein. The specification CC describes phosphorylation-independent arrestin mutants. These mutants are cused in screening assays to identify ligands and/or modulators of GC used in screening assays to identify ligands and/or modulators of GC protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand CC comprises contacting a composition comprising the GPCR and a CC constitutively active arrestin mutant with a test compound; and CC determining the ability of the test compound to modulate binding of CC arrestin mutant to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is used for identifying CC potential ligands and/or modulators of GPCRs, particularly modulators, CC for use as human therapeutics. Modulators of GPCR may be used for CC treating patients bindings, retinitis pigmentosa, stationary night CC bindness, colour bindness, nephrogenic DI, isolated glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial hypocalciuric hypercalcemia, hyperparathyroidism and neurological disorders. The CC methods may be used for screening pluralities of test compounds (e.g. a Small molecule library of compounds) or a composition containing a contentification of factural and surrogate agonists of orphan GPCRs, and for identification of factural and surrogate agonists of orphan GPCRs, and for identification of factural and surrogate agonists of orphan GPCRs, and for identification of factural and surrogate agonists of orphan GPCRs, and for identification of factural and surrogate agonists of orphan GPCRs, and for identification of factural and surrogate agonists of orphan GPCRs, and for identification of factural and surrogate agonists of orphan GPCRs, and for identification of factural and surrogate agonists.
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retinitis pigmentosa, color blindness or neurlogical disorders, uses
phosphorylation-independent arrestin mutants particularly suited for in
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The invention discloses a composition comprising two or more isolated rat corrivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cin comprising the vector, a method for identifying a nucleotide sequence. Also comprising the vector, a method for identifying a nucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially regulated in an animal subjected to pain and a that is differentially expressed in neuronal tissue of a first animal composition of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the polynucleotide sequence compound that regulates the activity of one or more of the polynucleotides, a method for join, a method for identifying a compound of a compound or small molecule that regulates the activity of one or more of the polynucleotide sequence of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating completions, a method for identifying a compound useful in treating the polynucleotide or their antibodies. The polynucleotide or the compound that injury (CCI) and spared nerve injury (Chung), chronic constriction the specification, which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed of the printed in the polynucleotide or the printed of the printed during pain. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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01-NOV-2001; 2001US-0346382P
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BAYER AG.
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segmental nerve injury; chronic constriction injury; CCI;
nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                        Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI;
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                                                                                                                                                                        D'urso D,
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CC claimed are a vector comprising the novel polynucleotide, a host cell CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence contains the vector comprising the vector comprising the vector. The notation of the polynucleotide sequence contains the vector and a property of the compound which regulates the compound that is differentially expressed in neuronal tissue of a first animal compound which regulates the expression of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the composition. The polynucleotides given in the composition and a pharmaceutical composition composition composition and a pharmaceutical composition composition in treating composition and a pharmaceutical composition composition composition that regulates the polypeptides or their antibodies. The polynucleotide given in the composition composition composition composition composition composition composition composition composition composition for a serior in the compound that serior activity is useful for preparing a medicament for treating composition co The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal. Claim 1; Page; 1017pp; English. rat

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This invention relates to a method of differentially modulating the CC growth or differentiation of blood endothelial cells (BEC) or lymphatic cc endothelial cells (EEC) comprises contacting endothelial cells with a CC composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises CC identifying a human subject with lymphoedema and with a mutation in at CC identifying a human subject with lymphoedema and with the proviso that CC correlates with lymphoedema in human subjects, and with the proviso that CC correlates with lymphoedema in human subjects, and with the proviso that CC correlates with lymphoedema in human subjects, and with the proviso that CC composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, CC vasotropic or antiinflammatory activity or for gene therapy. The method CC is useful in modulating the growth or differentiation of blood condothelial cells or lymphatic endothelial cells, in treating hereditary CC prodisposition to the disorder or an endothelial cell disorder or condothelial cells in manufacturing a medicament for the differential modulation of blood vessel endothelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table the specification) which is differentially expressed during pain. Not the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 173; 176pp; English
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                                              lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed protein which is related to the method of the invention Note: This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification.
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WO200253726-A2 domain; SID,

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N-PSDB; ABS51032

Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders.

Claim 1; Page 53; 125pp; English.

The invention relates to a complex of protein-protein interactions (forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polynucleotides in adipocyte cells as for the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for the recombinant host cell which is transformed with two vectors, where the first vector comprises a polynucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polynucleotide encoding a second hybrid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the

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            The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, cc claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide, a host cell cc which is differentially regulated in an animal subjected to pain and a vector comprising the novel polynucleotide sequence (cc which is differentially regulated in an animal subjected to pain and a cc that increases or decreases the expression of the polynucleotide sequence cc that is differentially expressed in neuronal tissue of a first animal cc compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the composition, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a composition, a method for identifying a composition, a method for identifying a composition, a method for identifying a composition, a method for identifying a composition, a method for identifying a composition, a method for identifying a composition, a method for identifying a composition, a method for identifying a composition, a method for identifying a composition, a method for identifying a composition, a method for identifying a composition.
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                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising two or mopreparing a medicament for treating
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also comprising the vector comprising the novel polynucleotide a host cell which is differentially regulated in an animal subjected to pain and a that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide agent subjected to pain, a method for identifying an agent state is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying an agent of the polynucleotide sequence.
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GENBANK; P29067.
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CC the expression of a polynucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a CC compound that regulates the activity of one or more of the CC polynucleotides, a method for producing a pharmaceutical composition, a CC method for identifying a compound or small molecule that regulates the CC activity in an animal of one or more of the polypeptides given in the CC specification, a method for identifying a compound useful in treating CC pain and a pharmaceutical composition comprising the one or more CC polypeptides or their antibodies. The polynucleotide or the compound that CC modulates its activity is useful for preparing a medicament for treating CC pain (e.g. spinal segmental nerve injury (Fung), chronic constriction CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene CC therapy). The sequence presented is a rat protein (shown in Table 2 of CC the specification) which is differentially expressed during pain. Note: CC The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic form directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences.
Sequence 410 AA;
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Search completed: February 9, Job time : 166 secs 밁 ঠ Matches Query Match Best Local & 341 ELPFVLMHPKP 351 |||||||| 340 ELPFVLMHPKP 350 tch 2.9%; Score 11; DB 7; Length 410; al Similarity 100.0%; Pred. No. 0.11; 11; Conservative 0; Mismatches 0; Indels 2005, 23:58:30 °; Gaps

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US-09-880-137-8
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Best Local :
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4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
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1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8		1.8		1.8	1.8	1.8	1.8	1.8	1.8	1.8
70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70
W	w	w	W	w	w	W	w	w	w	w	w	W	ω	w	w	w	ω
67-953B-	US-09-367-953B-85	US-09-367-953B-84	US-09-367-953B-83	US-09-367-953B-82	US-09-367-953B-80	US-09-367-953B-78	US-09-367-953B-76	US-09-367-953B-75	US-09-367-953B-74	US-09-367-953B-72	US-09-367-953B-71	US-09-367-953B-70	US-09-367-953B-68	US-09-367-953B-65	US-09-367-953B-55	US-09-367-953B-52	US-09-367-953B-31
, 98	Sequence 85, Appl	•	•	Sequence 82, Appl	•	•	-	-	-	-	•	Sequence 70, Appl	68,	•	e 55,	•	Sequence 31, Appl

ALIGNMENTS

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Sequence 4, Application US/09880137

Patent No. 6640025

GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
ITILE OF INVENTION: METHODS OF ASSAYING FOR G
ITILE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131

CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US/09/880,137

CURRENT FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRSUSEQ for Windows Version 4.0

SEQ ID NO 4
LENGTH: 409

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
FILE REPERENCE: MNI-131
CURRENT FILING DATE: 2001-03-05
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOUTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09880137
Patent No. 6640025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: Description of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 ELPFYLMHPKP 351
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; ORGANISM: Homo sapiens US-09-880-137-4

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GENERAL INFORMATION:

APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
FRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
OFFWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 388
TYPE: PAT
ORGANISM: Homo sapiens
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US-09-880-137-5
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Patent No. 6640025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.0%; P
Matches 11; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US/09/880,137
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR APPLICATION NUMBER: US 60/186,706
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
1.ENGTH: ANG
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Patent No. 6640025
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ORGANISM: Artificial Sequence
FEATURE:
                                                             Local Similarity les 9; Conserv
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Best Local s
19 GKRDFVDHV
                     22 GKRDFVDHV 30
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                                                         Conservative
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27
                                           2.3%; Score 9; DB.,
100.0%; Pred. No. 2.;
vative 0; Mismatches
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Pred. No. 0.03;
0; Mismatches
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5. 2.5;
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                                                                      Length 388;
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                                           Indels
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Sequence 27414, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/274,788
PRIOR APPLICATION NUMBER: US/09/094,190
NUMBER OF SEQ ID NO3: 33142
FENGTH: 279
TYPR: DPT
RESULT 7

US-09-349-016-9940
; Sequence 9940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION UNDER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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Best Local
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09880137
Patent No. 6640025
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MMI-131
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nes 8; Conserv
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TYPE: PRT
                                                                                                                                                                                                                                                                                                          336 GELSAELP 343
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ilarity 100.0%; Pred. No. 17,
Conservative 0; Mismatches
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Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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Sequence 8384, Application US/09949016
; Patcent No. 6812339
; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF PILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-40-14
; PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/277,768
PRIOR APPLICATION NUMBER: 60/277,768
PRIOR APPLICATION NUMBER: 60/271,759
PRIOR APPLICATION NUMBER: 60/271,768
PRIOR APPLICATION NUMBER: 60/271,768
PRIOR APPLICATION NUMBER: 60/271,768
PRIOR APPLICATION NUMBER: 60/271,768
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOPTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 8383
LENGTH: 401
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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; ORGANISM: Human
US-09-949-016-9940
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APPLICANT: VENTER, J.
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-09-949-016-8383
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Best Local &
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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PRIOR FILING DATE: 2000-10-20
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100.0%; Pred. No. 20
tive 0; Mismatches
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OF DETECTION
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FILE REFERENCE: MVI-131
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 418
TYPE: PRT
ORGANISM: Bos taurus
US-09-880-137-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8384
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; TYPE: PRT
; ORGANISM: Homo s
US-09-880-137-3
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Best Local S
Matches 8
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09880137
Patent No. 6640025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09880137
Patent No. 6640025
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8384
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Best Local
                              Query Match
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CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
                                                                                                                                                                                                                                               APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-09-08
Local Similarity 100.0%;
nes 8; Conservative (
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nes 8; Conserv
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nes 8; Conserv
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            Score 8; pred. No
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Pred. No.
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red. No. 25
Mismatches
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      DB . 25;
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: POTTER, Jane E. R.
                                                                                                                                                                  COMPUTER REALBLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
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i TYPE: PRT
i ORGANISM: Homo sapiens
US-09-880-137-2
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Best Local Similarity 100.0%; Pred. No
Matches 8; Conservative 0; Mismat
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PRIOR APPLICATION DATA:
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US-09-880-137-2
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atent No. 5976551
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mottez, E
APPLICANT: Abastado,
APPLICANT: Kourilsky
TITLE OF INVENTION: (
TITLE OF INVENTION: (
TITLE OF INVENTION: (
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                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 05-DEC-1991
                                                                                                                                                                                                                                                                               STATE: D.C.
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
NUMBER: OF SEQ ID NOS: 8
NUMBER: OF SEQ ID NOS: 8
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, ......
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
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TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
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Kourilsky, Philippe
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                                                                                                                                                                                                                                                                                                                                                Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                               07-JUNE-1995
N: 530
                                                                                                                                                                                                                                                                                                                                                                                                  An Altered Major Histocompatibility Complex(MHC) Determinant and Methods for Using the
                                                                                                                US_07/801,818
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                                                                                                                                                                                                   Version #1.25
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; MOLECULE TYPE: US-08-481-985B-28
Query Match
                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
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                                                                                                                            NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202,4804
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin ReleacTURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 07-UNN-199;
CLASSIFICATION: 435
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                                                 TYPE: ami
                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NIMMER OF CONTROLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1300 I St
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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                                                           amino acid
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                                                                        15 amino acids
                                                                                                                   202-408-4400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08481985B
                                                                                                                                                                                                                                    15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995
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%; Pred. No. 12;
0; Mismatches
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1.8%;

Score 7;

DB 3;

Length 15;

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Gazrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE: 07-SEP-193
APPLICATION NUMBER: US/08/370,476
FILING DATE: 07-SEP-193
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-193
APPLICATION NUMBER: US 08/072,787
FILING DATE: 05-DEC-1991
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
APPLICATION NUMBER: US 07/92,473
FILING DATE: 05-DEC-1991
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELEPMONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
                                                                                                                                                           ; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-370-476-28
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US-08-370-476-28
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                                                                          Query Match 1.8%; Score 7; DB 3; Best Local Similarity 100.0%; Pred. No. 12; Matches 7; Conservative 0; Mismatches
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Patent No. 6153408
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%; Pred. No. 12; Matches 7; Conservative 0; Mismatches
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 127
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                                      256 LETSEGC 262
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Abastado, Jean-Pierre
Kourilsky, Phillipe
Lone, Yu-Chun
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Search completed: February 10, 2005, 00:11:11 Job time : 44 secs

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Minimum |
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Perfect score:
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seq length: 2000000000
Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

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1 MVYNFKVFKKCAP
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 4 4 4 4 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1	Regult No.
383 383 111 111 111 111 111 111	Score
100 100 100 100 100 100 100 100 100 100	Query Match
383 383 398 398 400 400 400 8866	Query Match Length DB
14 14 14 10 14 10 10 10 10	BB
US-10-094-240-2 US-10-056-405-2 US-09-880-137-8 US-09-800-137A-8 US-09-800-137A-9 US-10-094-240-27 US-09-880-137-7 US-09-880-137-7 US-09-800-137A-7 US-09-800-137A-7 US-09-800-137A-7 US-09-800-137A-7 US-10-038-010-54 US-09-800-137-5 US-10-722-357-31 US-09-880-137-5	ID
Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli Sequence 8, Appli Sequence 25, Appli Sequence 27, Appli Sequence 4, Appli Sequence 7, Appli Sequence 7, Appli Sequence 4, Appli Sequence 54, Appli Sequence 54, Appli Sequence 54, Appli Sequence 54, Appli	Description

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-10-424-599-267	0010	-10-446-2	39-3132	0-062-7	-10-282-122A-67		-10-437-963-11432	-10-437-963-172	-10-038-010	0-335-977-7	US-10-282-122A-58890	15-242-11	-10-043-487-34	-60	-09-800-137A-	880-1	US-09-880-137-1	-09-800-137	0	0-335-977-	-10-767-701-3	10-424-	-10-106-698-	-10-767-701-	77-	0-424-599-14820	US-10-424-599-154582	64-761-4076	-09-800-	7	US-09-880-137-6
Sequence 267779,	O	O	Ø	ø	æ	o o	е Ц	0 1	e 52, Ap	(D	e 5889	115	e 34	e 2,	e 1,	2	<u>ب</u>	e 3,	3, Appl	e 75	Sequence 38282, A	e 224408	e 4673,	о Д	e 7580,	e 14820	e 1545	4076	e 6, Appl	e 5,	6, 7

ALIGNMENTS

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-094-240-2
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                                                                                                                                                                                                                                                   Query Match 100.0%; Score 383; I
Best Local Similarity 100.0%; Pred. No. 0;
Matches 383; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/094,240
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
FILE REFERENCE: N8289
121 PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
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                                                                                             FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPPTFNIS 120
                                                                                                                                                                                          MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
                                                                     FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120
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RESULT 2
US-10-056-405-2
; Sequence 2, Application US/10056405
; Publication No. US20030166013A1
; GENERAL INFORMATION:
; APPLICANT: ZMIEBEL, LAURENCE J.
; TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS OF FILE REFERENCE: N964
; TITLE OF INVENTION: USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/056,405
; PRIOR APPLICATION NUMBER: US/10/056,405
; PRIOR APPLICATION NUMBER: 00/264,649
; PRIOR FILING DATE: 2001-01-26
; SOFTWARE: PATCHING DATE: 201-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Anopheles gambiae US-10-056-405-2
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Best Local Similarity
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                         361
                                              361 DSQADVETFRQDTIDQQASVDFE 383
                                                                                                                                               301 CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA 360
                                                                                                                                                                                                                                                                                241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLQXVMYLTPLLSSNKQRRGIALDGQIKRQDQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FRYGREDEVMGLNFÓKELŐLÁSEQIYPRPEKSDKEÓTKLÓEKLLKKLGSNÁIPFTFNÍS
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                                                                                                           CLASTTĹĹAĢÞÓŖŔĎÁÞĠŸĬĬSŸAŸĸŸĸĹŦĹĠĀĹĠĠĖĹŚĀĖĹÞŦŸĹMŀPĸPĠTĸĀĸŸĬŀĄ
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RESULT 5
US-10-094-240-25

Sequence 25, Application US/10094240

Publication No. US20030082637A1

GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.

TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE,
FILE REFERENCE: N8289
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Sequence 8, Application US/09880137

GENERAL INFORMATION:

APPLICANT: Berstein, Gabriel

TITLE OF INVENTION: METHODS OF ASSAYING FOR G

FILE REFERENCE: MNI-131

CURRENT APPLICATION NUMBER: US/09/880,137

PRIOR APPLICATION NUMBER: US/09/880,137

PRIOR APPLICATION NUMBER: US 60/186,706

PRIOR APPLICATION NUMBER: US 60/186,706

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 382

TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION UNMEER: US/09/800,137A
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
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Best Local Similarity
Matches 11; Conserve
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US-09-880-137-8
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TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
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Best Local (
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100.0%; Pred. No.
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                                                            AND METHODS OF USE THEREOF
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CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 27
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 398
TYPE: PRT
ORGANISM: Anopheles gambiae
US-10-094-240-25
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-4
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US-10-094-240-27
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US-10-094-240-27
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Patent No. US20020031295A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
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Matches
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SEQ ID NO 27
LENGTH: 401
TYPE: PRT
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Best Local Similarity 100.0%;
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/880,137 CURRENT FILING DATE: 2001-03-05
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CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR FILING DATE: 2002-01-24
                                                                                          PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FABLSEQ for Windows Version 4.0
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TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE,
FILE REFERENCE: N8289
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Sequence 4, Application US/09800137A

Publication No. US20030157553A1

APPLICANT: Berstein, Gabriel

APPLICANT: Berstein, Gabriel

TITLE OF INVENTION: METHODS OF ASSAYING FOR G

TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIC

FILE REFERENCE: MNI-131

CURRENT APPLICATION NUMBER: US/09/800,137A

CURRENT FILING DATE: 2001-03-05

PRIOR APPLICATION NUMBER: US 60/186,706

PRIOR PILING DATE: 2000-03-03
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                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-137A-4
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                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09880137
Patent No. US20020031295A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
                                                                     Matches
                                                                              Query Match
Best Local Similarity
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: MNI-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                341 ELPFYLMHPKP 351
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 ELPFVLMHPKP 349
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Conservative
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0; Mismatches
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Pred. No. 0.11;
                                                                                   Score 11;
Pred. No.
                                                                     Mismatches
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RESULT 10

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Sequence 31, Application US/1072
Publication No. US20040191803A1
GENERAL INFORMATION:
APPLICANT: GALLAGHER, MICHELA
APPLICANT: LUND, PAULINE KAY
APPLICANT: ROTHSTEIN, JEFFREY
                                                                                                          RESULT 12
US-10-722-357-31
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TITLE OF INVENTION: METHODS OF ASSAYING FOR G

TITLE OF INVENTION: METHODS OF ASSAYING FOR G

FILE REFERENCE: MNJ-131

CURRENT APPLICATION NUMBER: US/09/800,137A

FRIOR APPLICATION NUMBER: US/09/800,137A

FRIOR APPLICATION NUMBER: 03-05

PRIOR FILING DATE: 2001-03-05

PRIOR FILING DATE: 2000-03-03

SOFTWARE: FASC ID NOS: 8

SOFTWARE: FAST OF SEQ ID NOS: 8

LENGTH: 409

TYPE: PRT

OPCANISM. APTIFICIAL COMMENCE.
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Best Local Similarity
Matches 11; Conserv:
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FEATURE:
NAME/KEY: beta Arrestin2
LOCATION: (1)...(410)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-038-010-54
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/259,377
RIUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
LENCTH: 410
TYPE: PRT
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Best Local Similarity
Matches 11; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
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Sequence 7, Application US/09800137A

Publication No. US20030157553A1
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LUND, PAULINE KAY
ROTHSTEIN, JEFFREY
                                                                 Application US/10722357
to. US20040191803A1
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    LENGTH: 388
    TYPE: PRT
    ORGANISM: Homo sapiens
    US-09-880-137-6

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Patent No. US20020031295A1

GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
ITILE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILL REFERENCE: MAI-131
CURRENT APPLICATION NUMBER: US/09/880,137
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR APPLICATION NUMBER: US 60/186,706
INUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                    APPLICATION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILE REFERENCE: MNI-131
CURRENT FILING INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISION INVISIONI INVISIONI INVISIONI INVISIONI INVISIONI INVISIONI INVISIONI INVISIONI INVISIONI INVISIONI IN
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US-09-880-137-6
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/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-137-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09880137 Patent No. US20020031295A1 GENERAL INFORMATION:
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Best Local S
Matches 9
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US-09-880-137-5
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; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-722-357-31
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CURRENT APPLICATION NUMBER: US/10/722,357
CURRENT FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: 60/413,152
PRIOR FILING DATE: 2002-11-22
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 3.2
THYRM:
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les 9; Conserv
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100.0%; Pred. No. 8.
vative 0; Mismatches
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RESULT 15

US-09-800-137A-5

# Sequence 5, Application US/09800137A

# Publication No. US20030157553A1

# Publication No. US20030157553A1

# GENERAL INFORMATION:
### APPLICANT: Berstcin, Gabriel

### TITLE OF INVENTION: METHODS OF ASSAYING FOR G

### TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS

### FILE REFERENCE: MNI-131

### CURRENT FILLING DATE: 2001-03-05

### CURRENT FILLING DATE: 2001-03-05

### PRIOR APPLICATION NUMBER: US 60/186,706

### PRIOR APPLICATION NUMBER: US 60/186,706

### PRIOR APPLICATION NUMBER: US 60/186,706

### PRIOR PILING DATE: 2000-03-03

### WUMBER OF SEQ ID NOS: 8

### SOPTWARE: FASTSEQ for Windows Version 4.0

### SEQ ID NO 5

### LENGTH: 388

### TYPE: PRT

### ORGANISM: Homo sapiens

US-09-800-137A-5
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Search completed: February 10, 2005, 00:13:29 Job time : 132 secs
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19 GKRDFVDHV 27
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Result
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nd Head; PubMed=11822731; nazza F., Costant	(Africa ; Arthr ygota;		INARY;		143 147	141 142	1773	412 470	394	392	392 202	388	359	147	
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822731; Costantini C., Favia G.;	gambiae (African malaria mosquito). Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles =7165;	Created) Last sequence update) Last annotation update)	PRT; 383 AA.	ALIGNMENTS	O48243 O48246	048240 048239	Ö82745	Q641D8 Q9V393	Q7YS78	Q9PTE7	Q9N0H5	ARRC_HUMAN	Q96EN2	Q6WGR2	
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Pfam; PP02752; Arrestin_N; 1.
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PROSITE; PS00295; ARRESTIN.
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proc. Natl. Acad. Sci. U.S.A. 99:1633-1638(2002).
EMBL; AJ014409; CAC39103.2; -.
EMBL; AY017417; AAG54081.1; -.
HSSP; P17870; 1G4M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular characterization and chromosomal mapping of transcripts having tissue-specific expression in the malaria mosquito anopheles gambiae: possible involvment in visual or olfactory processes."; parasitol. Res. 88:1-8(2002).
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
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ENSANGP00000012569 (Fragment).
Anophales gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                   AAAB01008980; EAA13874.2; -. P17870; 1G4M.
                                                FRYGREEDEVMGINFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS
 PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                                                                                                                                   Similarity
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                                 PRYGRÉEDEVMGLNFOKELCLASEQIYFRPEKSDKEOTKLOEKLLKKLGSNAIPFTFNIS
                                                                                         MYNEKVEKKCAPNGKVTLYMGKRDEVDHVSGVEDIDGIVVLDDEYIRDNRKVFGQIVCS
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100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                                                                                                             245
245 AA;
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STRAIN-4ARR, Yaounde, and L3-5;

Morlais I., Poncon N., Simard F., Cohuet A., Font Morlais I., Poncon N., Simard F., Cohuet A., Font R., Morlais I., Poncon N., Simard F., Cohuet A., Font R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March R., March
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GO; GO:0007165; P:signal transduction; IE
InterPro; IPR000658; Arrestin.
InterPro; IPR011022; Arrestin.
InterPro; IPR011021; Arrestin.
PEam; PP02752; Arrestin.
Pfam; PF00339; Arrestin.N; 1.
PRINTS; PR00309; Arrestin.N; 1.
PRINTS; PR00309; Arrestin.; 2.
PRODOM; PD002099; Arrestin; 2.
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Anopholes gambiae (African malaria mosquito).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Ano, CBI_TaxID=7165,
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                                          121
                                                                                                                   YRNTVASLETSEGCFIQFGSSLQKVMYLTFLLSSNKORRGIALDGQIKRQDQCLASTTLL
                                   YRNTVASLETSEGCETQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLASTTLL 308
                                                                                                                                                                                                                                                        LQQGBDDNGDÞCGVSYYVKÍFAGESETDRTHRRSTVTLGÍRKÍQFAÞTKQGQQPCTLVRK
                                                                                                                                                                                                                                                                                           LQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTLVRK 188
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; 27038 MW; 86D8F4520115DASF CRC64;
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100.0%; Pred. No. 1.3e-236;
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Last annotation updat
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RESULT QUESTION ACCORDED TO 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 101 DOT 10
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P15372; Q9VJA8;
01-APR-1990 (Rel
                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
25-JAN-2005 (Rel. 46, Last annotation update)
Phosrestin II (Arrestin A) (Arrestin 1).
Name-Arr1; Synonyms-ArrA; ORFNames-CG5711;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroides; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ascalaphus macaronius.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Neuroptera; Ascalaphidae;
NCBI TaxID=146496;
  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDINE-90139925; PubMed=1689056;
Smith D.P., Sheih B.-H., Zuker C.S.;
"Isolation and structure of an arrestin gene fro Proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990)
                                                                                                                                                                                                                                                                                                                                                                                                       DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02752; Arrestin_C; 1.
Pfam; PF00339; Arrestin_N; 1.
PRINTS; PR00309; ARRESTINS; 1.
PROSITE; P800295; ARRESTINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GG; GO:0007600; P:sensory perception; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR000698; Arrestin.
InterPro; IPR011022; Arrestin_C.
InterPro; IPR011021; Arrestin_N.
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EMBL, AJ303080; CAC116(2001).
EMBL, AJ303080; CAC36938.1; -.
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         RX MEDLINE-2019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Champe M., Pfeiffer B.D., Hrandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelaon C.R., Miklos G.L.G., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelaon C.R., Miklos G.L.G., RA Man M.H.J., P., Agbayani A., An H.-J., Andrews-Pfannkoch C. Baldwin D., Baselev R.G., Champe M., Pfeiffer B.D., Bandari D., Bolshakov S., R. Beeson K.Y., Benos P.V., Bermann B.P., Bandari D., Bolshakov S., R. Berok D., Bendari D., Bolshakov S., R. Berok D., Schampe P.V., Bermann B.P., Bandari D., Bolshakov S., R. Berok D., Schampe P.V., Bermann B.P., Bandari D., Bolshakov S., R. Borkeva D., Botchan M.R., Bouck J., Brokstein P., Brottler P., R. Charty J.M., Cavley S., Dahlke C., Davenport L.B., Davies P., R. Bastis K.C., Busam D.A., Butler H., Gadieu E., Center A., Chandra I., R. Gebon K.J., Brownes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rosley S., Dahlke C., Davenport L.B., Davies P., R. Dowles P., Garg N.S., Gebbart W.M., Glasser K., R. Dowles B., Delicher A., Deng Z., Mays A.D., Davie D.C., Dunn P., Ra Horston K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., R. Armeris M.L., Harris M.L., Harris M.L., Garg N.S., Gebbart W.M., Glasser K., R. Posler C., Gabrielian A.E., Garg N.S., Gebbart W.M., Glasser K., R. Armeris N.L., Harris M.J., Hernan T.J., Hernandez J.R., Houck J., Hostin D., Harris M.J., Harris M.J., Ketchum K.A., Kamel B., Kolish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kamel B., Kolish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lid X., Matter B., McLecd M.P., McLecd M.P., McLecd M.P., McLecd M.P., McLecd M.P., McLecd M.P., McLe
                              Genome
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MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokst
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                                                                   George R.A., Guarin H., Kronmiller B., F
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.
                                                                                              MEDILINI-- Stapleton M., Caliv. Stapleton M., Guarin H.,
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Hyde D.R., Mecklenburg K.L., Pollock J.A., Vihtelic T.S.,
"Twenty Drosophila visual system cDNA clones: one is a ho
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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      PHOSPHORYLATION
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                                                Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002)
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InterPro; IPR01022; Arrestin_C.

InterPro; IPR011021; Arrestin_C.

Refam; PF02752; Arrestin_N; 1.

Pfam; PF02339; Arrestin_N; 1.

PRINTS; PR00339; ARRESTIN; 2.

PRINTS; PR002099; ARRESTIN; 2.

PROSITE; PS00295; ARRESTINS; 1.

Phosphorylation; Sensory transduction; Vision.

SEQUENCE 364 AA; 40771 MW; ODCC764C4F890FC2 CRC64;
                                 Q7YTV9
Q7YTV9
Q7YTV9;
01-OCT-2003 (TrEMBLrel
01-OCT-2003 (TrEMBLrel
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Arrestin (Fragment).
             Name=arr1;
Anopheles :
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EMBL; M30140; AAA28380.1; -
EMBL; AB003657; AAE33644.1; -
EMBL; AV061824; AAL27635.1; -
PIR; A34867; A34867.
HSSP; P17870; 1G4M.
IntAct; P15372; -
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GO: GO:0005524; C:membrane fraction; IDA.
GO: GO:0016028; C:rhabdomere; IDA.
GO: GO:0016060; P:metarhodopsin inactivation; IGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 260:1910-1916(1993).

-!- FUNCTION: Regulates photoreceptor cell deactivation. Arr. proteins are mediators of rhodopsin inactivation and are for the termination of the phototransduction cascade. Photoreceptors. Inner and outer segments, and the inner regions of the retina.

-!- PTM: Phosphorylated, but does not undergo light-induced
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Zuker C.S.;
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Matsumoto H., Yamada T.;
"Phosrestins I and II: arrestin homologs which undergo differential
light-induced phosphorylation in the Drosophila photoreceptor in
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SIMILARITY: Belongs to the arrestin family.
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stephensi (Indo-Pakistan malaria mosquito).
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.nathan R., Colley N.J., Hardy R.W., Socolich M.,
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FRAVIA G., ricci I., Casiraghi M., E.
FRAVIA G., ricci I., Casiraghi M., E.
Submitted (FEB-2003) to the EMBL/Ge.
EMBL; AJS44225; CAD6650.1; -.
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SEQUENCE 18 AA; 2075 MW; A273A3
                                  EMBL; AJ544224; CAD66649.1;
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SEQUENCE 18 AA; 2075 MW;
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                                                                                                               Anopheles arabiensis (Mosquito).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=7173;
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Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera, Endopterygota, Diptera, Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=221566;
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Favia G., ricci I., Casiraghi M., Esposito F.;
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EMBL; AJ544226; CAD66551.1; -.

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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles
NCBI TaxID=30069;
   Similarity
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                                                                                                                                                                                                                                                                                                                         Conservative
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                                                              Casiraghi M., Esposito F., to the EMBL/GenBank/DDBJ
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InterPro; IPRO11022; Arrestin C.
InterPro; IPRO11021; Arrestin N.
Pfam; PP002752; Arrestin C; 1.
Pfam; PP00339; Arrestin N; 1.
PRINTS; PR00309; ARRESTIN.
PRODOM; PD002099; ARRESTIN; 2.
PROSITE; PS00205; ARRESTINS; 1.
Sensory transduction; Vision.
SEQUENCE 363 AA; 40680 MW; 7C3
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P55274;
01-OCT-1996
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01-OCT-1996
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Heliothis virescens (Noctuid moth) (Owlet moth) Eukaryota; Metazoa; Arthropoda; Hexapoda; Insec Neopeera; Endopterygota; Lepidoptera; Glossata; Noctuidae; Heliothinae; Heliothis.
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01-OCT-1996 (Rel. 34, Last
15-JUL-1999 (Rel. 38, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X79072; CAA55672.1; -. PIR; A55081; A55081. HSSP; P17870; 1G4M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1996 (Rel. 34, Last seq
05-JUL-2094 (Rel. 44, Last ann
Phosrestin II (Arrestin A) (Ar
                                                                                                  Arrestin homolog.
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Hexapoda; Insecta; Pterygota;
a; Brachycera; Muscomorpha; Oestroidea;
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ssata; Ditrysia; Noc
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Q5.JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to Drosophila melanogaster CG5711 (Fragment).
Drosophila yakuba (Fruit fly).
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MEDLINB=22887302; PubMed=14525923; DOI=10.1101/gr.1311003;
Domazet-Logo T. Tautz D.;

"An evolutionary analysis of orphan genes in Drosophila.";
Genome Res. 13:2213-2219(2003).
EMBL; AY232006; AR310029.1; -.

HSSP; P08168; 1AYR.
  ARRH_LIMPO
P51484;
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NON_TER 1 1
NON_TER 52 52
SEQUENCE 52 AA; 6166 MW;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00309; ARRESTIN.
ProDom; PD002099; Arrestin; 2.
PROSITE; PS00295; ARRESTINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR011021; Arrestin
Pfam; PF02752; Arrestin_C; 1.
Pfam; PF00339; Arrestin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; B56607; B56607.
HSSP; P17870; 1G4M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B; Raming K., Frektag J., Krieger J., Breer H.; "Arrestin-subtypes in insect antennae."; Cell Signal 5:69-80(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6XI26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro; IPR011022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - SIMILARITY: Belongs to the arrestin family
                                                                                                                                                                                                                                                                  l Similarity
14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                μ
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                                                                                                                                                                                                VEPIDGIVVLDDEY 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MVYNFKVFKKCAPNGK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVYNFKVFKKCAPNGK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 AA;
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.2%; or.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42747 MW; 84BB92B1BB3DA573 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arrestin_C.
Arrestin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arrestin.
                                                                                                                                                                                                                                                                                                                      3.7%;
                                                                                                                                                            46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16;
Pred. No.
                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                             Score 14; DB 2; pred. No. 1.2e-
                                                                                                                                                                                                                                                                                                                                                                          081C148570B5EB6F CRC64;
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                                                                                                                                                                                                                                                                     Mismatches
                              400
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                                                                                                                                                                                                                                                                                             1.2e-05;
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                                                                                                                                                                                                                                                                                                                   Length 52;
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RESULT
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RESULT 13
ARRH_LOCMI
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Best Local S
Matches 13
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HSSP; P17870; 1G4M.
InterPro; IPR000698; Arrestin.
InterPro; IPR011022; Arrestin.C.
InterPro; IPR011021; Arrestin.C.
Pfam; PF02752; Arrestin.C.; 1.
Pfam; PF0275339; Arrestin.W; 1.
TISSUE-Antenna;

MEDLINE-9319955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;

Raming K., Freitag J., Krieger J., Breer H.;

"Arrestin-subtypes in insect antennae.";

Cell. Signal. 5:69-80(1993).

-!- SIMILARITY: Belongs to the arrestin family.
                                                                                                                                                                                                                                 ARRH LOCMI
P32122;
01-OCT-1993
                                                                                                                           Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Ac
Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                           SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=7004;
                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence up
15-UUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                          Arrestin homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Se
SEQUENCE 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00309; ARRESTIN.
ProDom; PD002099; Arrestin; 2.
PROSITE; PS00295; ARRESTINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMMBL outstation the European Bioinformatics Institute. There are no restrictions on it modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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Smith W.C., Greenberg R.M., Calman B.G.,
Donoso L.A., Battelle B.-A.;
"Isolation and expression of an arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Arrestin, lateral eye.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lateral eye.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Limulus polyphemus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurochem. 64:1-13(1995).
- FUNCTION: Plays an impor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: Phosphorylated.
SIMILARITY: Belongs to the arrestin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transduction.
                                                                                                                                                                                                                                                                                                                                             61 FRYGREEDEVMGL
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                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                           FRYGREEDEVMGL
                                                                                                                                                                                                                                                                                                                                                                              3.4%; Silarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sensory transduction; Vision.
A; 44302 MW; F30D0D25BC2BEE33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an important
                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                sequence update)
                                                                                                                                                                                                                                                                                                                                                                          Score 13; DB 1; Le; Pred. No. 0.00065; 0; Mismatches 0;
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                role
                                                                                                                                                                                                                                                        407
                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the photoreceptor
                                                                                                                                                                                                                                                      A
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from the
                                                                                                                                     1; Pterygota;
Acridomorpha;
                                                                                                                                                                                                                                                                                                                                                                          Indels
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MRL outstation -
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RESULT 15
Q66GU6
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Best Local Similarity
Matches 11; Conserv
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Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., I

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databa

EMBL; CR74921B; CAH18075.1; -

InterPro; IPR000698; Arrestin.

InterPro; IPR011022; Arrestin C.

Pfam; PF02752; Arrestin C.

Pfam; PF02752; Arrestin; 1.

ProDom; PD002099; Arrestin; 1.

ProDom; PD002099; Arrestin; 1.

ProDom; PD02109; Arrestin; 1.

ProDom; PD02109; Arrestin; 1.
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Best Local S
Matches 12
Q66GU6;
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Q68DZ5;
Q68DZ5;
Q68DZ5;
Q5-CCT-2004 (TrEMBLrel. 28, Created)
25-CCT-2004 (TrEMBLrel. 28, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686L0365;
Name=DKFZp686L0365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Endometrium;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00309; ARRESTIN, PRODOM; PD002099; ARRESTIN; 2. PROSITE; PS00295; ARRESTINS; 1. Sensory transduction. SEQUENCE 407 AA; 45543 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000698; Arrestin.
InterPro; IPR011022; Arrestin C.
InterPro; IPR011021; Arrestin_N.
Pfam; PP02752; Arrestin_C; 1.
Pfam; PP00339; Arrestin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the EMPL outstation the EMPL outstation its mon-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PIR; A56607; A56607.
HSSP; P17870; 1G4M.
                                                                                                                                          147
                                                                                                                                                                                     341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                        ELPFVLMHPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Similarity 100 12; Conservative
                                                                                                                                                                                ELPFVLMHPKP 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYGREEDEVMGL 73
                 PRELIMINARY;
                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                    2.9%;
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Primates;
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                                                                                                                                                                                                                                            Score 11; DB 2;
Pred. No. 0.039;
               PRT;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                61653F5BABCBB0FD CRC64;
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEC28A3A534935BB CRC64;
               398
            B
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0.0067;
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                                                                                                                                                                                                                                                                 Length 217;
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DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Arrestin 2-like protein Arr2.
GN Name-ARR2;
OS Anopheles gambiae str. PEST.
CC Name-ARR2;
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